

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 17, 2004, 15:21:58 ; Search time 94 Seconds
(without alignments)
1118.167 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSNGNQVRR.....KNSEINFSESFSSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : A_Geneseq_29Jan04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1951	100.0	372	5	Aae23954 PN7740 pr
2	1951	100.0	372	5	Abb79999 Human pro
3	1951	100.0	372	5	Abg70789 Fe65 inte
4	1951	100.0	372	5	Aae23953 PN7740 pr
5	1951	100.0	372	5	Abg70801 Fe65 inte
6	1951	100.0	372	5	Abg70826 Fe65 inte
7	1951	100.0	372	5	Abb07402 Human pro
8	1951	100.0	372	5	Aae23976 Human PN7
9	1951	100.0	372	5	Aae24078 Human PN7
10	1951	100.0	372	5	Aae14451 Human pro
11	1951	100.0	372	6	Abu10309 Human pro
12	1951	100.0	372	6	Aae23055 Human ser
13	1951	100.0	372	7	Abd66824 Human PN7
14	1951	100.0	372	7	Ad73452 Novel hum
15	1950	99.9	372	6	Ada54131 Human pro
16	1939	99.4	373	4	Aau29334 Novel hum
17	1924	98.6	373	3	AAE57077 Human pro
18	1809	92.7	351	5	Abb07401 Human pro
19	1727	88.5	352	5	Abb78059 Amino aci
20	1727	88.5	352	7	Ad31687 Human 161
21	1538.5	78.9	373	5	Abb07392 Human pro
22	1375.5	70.5	1072	4	Abg06716 Novel hum
23	1375.5	70.5	1195	4	Abg28412 Novel hum
24	1150	58.9	238	4	Aam41604 Human pol
25	951.5	48.8	233	4	Aab47431 Human pro

ALIGNMENTS

RESULT 1
AAE23954 standard; protein; 372 AA.

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Protein-protein interaction; neurodegenerative disorder; dementia;
Huntington's disease; Parkinson's disease; Alzheimer's disease; AD;
protein therapy; drug screening.

Unidentified.

WO200233114-A2.

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

QY 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLDPKKNLETLTLTAFLEIDKAFSSHARLSAD 180
 DB |||||
 QY 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLDPKKNLETLTLTAFLEIDKAFSSHARLSAD 180
 DB |||||
 QY 181 ATLLTSGTTATVALLRDGIELVVASVSDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 DB |||||
 QY 241 GGFVAVNSLGQPHVNGRLAMTRSIGDLDLKTSGVIAPEPKRIKLHHADDSFLVLTDDGI 300
 DB |||||
 QY 301 NFMVNSQIEICDFVNOCHDPNEAAHVAETQAIQYGTEDNSTAVVVPFGAWGKYKNSINF 360
 DB |||||
 QY 361 FSRSPASSGRWA 372
 DB |||||

RESULT 3

ID ABG70789 standard; protein; 372 AA.

XX AC

XX DT

XX DE 12-DEC-2002 (first entry)

XX DE Fe65 interacting human protein, PN7740, protein.

XX KW Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MLK2;
 mixed lineage kinase 2; ligand; transporter; cellular uptake;
 neuronal death; neurodegenerative disorder; Huntington's disease;
 Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS-1;
 PS2; Abeta; trophic; SAPP; metabolite; Fe65.

XX OS Homo sapiens.

XX PN US2002119927-A1.

XX PD 29-AUG-2002.

XX PF 09-OCT-2001; 2001US-00972757.

XX PR 17-OCT-2000; 2000US-0240790P.

XX PA (MYRI-) MYRIAD GENETICS INC.

XX PI Roch J, Bartel PL, Heichman K;

XX DR WPI; 2002-740204/80.

XX DR N-PSDB; ABS55204.

XX PT Modulating protein complex having proteins which is CIB interacting with
 mixed lineage kinase 2, in a cell, by administering compound that
 modulates the complex, or peptide that interferes interaction between
 proteins.

XX FS Example 6; Page 22; 37pp; English.

XX CC The invention discloses a method for modulating in a cell, a protein
 complex having a first protein, which is CIB (calcium-binding protein),
 interacting with a second protein, which is mixed lineage kinase (MLK)2,
 or the interaction of MLK2 with the ligand, which comprises administering
 to a cell a compound capable of modulating the protein complex or the
 interaction, or a peptide capable of interfering with the protein's
 interactions. The peptide is associated with a transporter capable of
 increasing cellular uptake of the peptide. The method is useful for
 modulating neuronal death in a patient having a neurodegenerative
 disorder such as Huntington's disease, Parkinson's disease, dementia and
 Alzheimer's disease. The technique used to discover additional proteins
 that interact with the major Alzheimer's disease proteins (including APP,

CC not defined, and presenilin) was the yeast two-hybrid system. CIB has
 been shown to interact with the presenilins, PS1 and PS2, but due to the
 casual role of mutations of these presenilins in Alzheimer's disease,
 other proteins, like MLK2, are likely to play a major role in the
 pathogenesis. APP metabolism is also a critical event in Alzheimer's
 disease pathogenesis as it leads to the release of either toxic (Abeta)
 or trophic (sAPP) metabolites. Fe65 (not defined) has been shown to
 interact with APP and peptides interacting with Fe65 may also be useful
 in treating neurodegenerative disorders. The compound may capable of
 strengthening the interaction between the first and the second protein.
 CC The sequence presented is the human PN7740 protein which was isolated due
 to its interaction with Fe65 found using the yeast two-hybrid system

XX SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;

Best Local Similarity 100.0%; Pred. No. 1.5e-206;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLQLDDRRVPTCHSSTSEPRCSRFPDGGSPAT 60

DB 1 MSTAALITLVRSQGNQVRRVLLSRLQLDDRRVPTCHSSTSEPRCSRFPDGGSPAT 60

QY 61 WDNFGIWDNRIDEPIILLPSIKYKPIPKISLNVGCSAQICKRKENEDRFPDQLTDEV 120

DB 61 WDNFGIWDNRIDEPIILLPSIKYKPIPKISLNVGCSAQICKRKENEDRFPDQLTDEV 120

QY 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLDPKKNLETLTLTAFLEIDKAFSSHARLSAD 180

DB 121 LYFAVYDGHGGPARADFCCHTHMEKICIMDLDPKKNLETLTLTAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVSDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

DB 181 ATLLTSGTTATVALLRDGIELVVASVSDSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLAMTRSIGDLDLKTSGVIAPEPKRIKLHHADDSFLVLTDDGI 300

DB 241 GGFVAVNSLGQPHVNGRLAMTRSIGDLDLKTSGVIAPEPKRIKLHHADDSFLVLTDDGI 300

QY 301 NFMVNSQIEICDFVNOCHDPNEAAHVAETQAIQYGTEDNSTAVVVPFGAWGKYKNSINF 360

DB 301 NFMVNSQIEICDFVNOCHDPNEAAHVAETQAIQYGTEDNSTAVVVPFGAWGKYKNSINF 360

QY 361 FSRSPASSGRWA 372

DB 361 FSRSPASSGRWA 372

RESULT 4

AAE23953 standard; protein; 372 AA.

XX AC

XX AC

XX DT 23-SEP-2002 (first entry)

XX DE PN7740 protein.

XX KW Protein-protein interaction; neurodegenerative disorder; CIB; MLK2;
 Alzheimer's disease; calcium binding protein; mixed lineage kinase 2;
 Huntington's disease; dementia; Parkinson's disease; AD.

XX OS Unidentified.

XX PN WO200233112-A2.

XX PD 25-APR-2002.

XX PF 16-OCT-2001; 2001WO-US032196.

XX PR 17-OCT-2000; 2000US-0240790P.

XX PA (MYRI-) MYRIAD GENETICS INC.

XX PI Roch J, Bartel PL, Heichman K;
 XX KW WPI; 2002-454607/48.
 XX DR N-PSDB; AAD38594.
 XX
 XX PT New protein complex comprising CIB and mixed lineage kinase 2, useful as
 XX targets for diagnostic tools in identifying individuals at risk for
 XX PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's
 XX PT disease or dementia.
 XX
 XX PS Example 6; Page 52; 91pp; English.
 XX
 XX The invention relates to the discovery of protein-protein interactions
 XX that are involved in the pathogenesis of neurodegenerative disorders
 XX including Alzheimer's disease (AD). The invention is also directed to
 XX protein complex comprising two proteins selected from a complex of
 XX calcium binding protein (CIB) and mixed lineage kinase 2 (MLK2). AD
 XX interacting proteins are useful as new targets for the identification of
 XX useful pharmaceuticals, new targets for diagnostic tools in the
 XX identification of individuals at risk, sequences for producing
 XX transformed cell lines, cellular models and animal models and new bases
 XX for therapeutic intervention in neurodegenerative disorders, including.
 XX Modulators of the protein complex are useful for treating
 XX neurodegenerative disorders including Huntington's disease, dementia,
 XX Parkinson's disease and AD. The present sequence is PN7740 protein. This
 XX sequence used in the exemplification of the invention
 XX
 XX Sequence 372 AA;
 XX
 XX Query Match 100.0%; Score 1951; DB 5; Length 372;
 XX Best Local Similarity 100.0%; Pred No. 1.5e-206;
 XX Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
 QY 61 WDNFGIWDNRIDEPILLPSPKIPKISLENVGCASQIGKRKENEDEFDFQAULTDEV 120
 Db 61 WDNFGIWDNRIDEPILLPSPKIPKISLENVGCASQIGKRKENEDEFDFQAULTDEV 120
 QY 121 LYFAVDGHHGGAADFCCHTHMEKIMDLKPKEKNLETLTLTFLAFLDKAFSSHARLSAD 180
 Db 121 LYFAVDGHHGGAADFCCHTHMEKIMDLKPKEKNLETLTLTFLAFLDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAVNSLQGVHNGRLAMTRISGLDLKTSQVIAEPETKRIKLHADDPSFLVLTGDI 300
 Db 241 GGFVAVNSLQGVHNGRLAMTRISGLDLKTSQVIAEPETKRIKLHADDPSFLVLTGDI 300
 QY 301 NFVWNSQEIICDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVPPGAKGKYKNSINFS 360
 Db 301 NFVWNSQEIICDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVPPGAKGKYKNSINFS 360
 QY 361 FSRSFASSGRWA 372
 Db 361 FSRSFASSGRWA 372
 RESULT 5
 ABG70801
 ID ABG70801 standard; protein; 372 AA.
 AC ABG70801;
 XX
 XX 16-DEC-2002 (first entry)
 XX
 XX Fe65 interacting human protein, PN7740, protein.
 XX

KW Yeast two-hybrid; PN7740; human; Mint2; PDE-9A; KIAA0427; ligand;
 KW transporter; cellular uptake; neuronal death; neurodegenerative disorder;
 KW Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease;
 KW APP; presenilin; Abeta; trophic; sAPP; metabolite; Fe65.
 OS Homo sapiens.
 XX
 XX US2002114799-A1.
 XX
 XX 22-AUG-2002.
 XX
 XX 10-OCT-2001; 2001US-00973077.
 XX
 XX 17-OCT-2000; 2000US-0240790P.
 XX (MYRI-) MYRIAD GENETICS INC.
 XX
 XX Roch J, Bartel PL, Heichman K;
 XX
 XX WPI; 2002-740090/80.
 XX N-PSDB; ABS55222.
 XX
 XX Modulating protein complex having Mint2 interacting with PDE-9A, by
 XX administering compound capable of modulating protein complex, or peptide
 XX capable of interfering with protein-protein interaction.
 XX
 XX Example 6; Page 22; 37pp; English.

CC The invention discloses a method for modulating in a cell, a protein
 CC complex having a first protein, which is Mint2, interacting with a second
 CC protein, which is PDE-9A, or the interaction of PDE-9A with the ligand,
 CC which comprises administering to the cell a compound capable of
 CC modulating the protein complex or the interaction, or a peptide capable
 CC of interfering with the protein's interactions. The peptide is associated
 CC with a transporter capable of increasing cellular uptake of the peptide.
 CC The method is useful for modulating neuronal death in a patient having a
 CC neurodegenerative disorder such as Huntington's disease, Parkinson's
 CC disease, dementia and Alzheimer's disease. The technique used to discover
 CC additional proteins that interact with the major Alzheimer's disease
 CC proteins (including APP, not defined, and presenilins) was the yeast
 CC hybrid system. Mint2 has been shown to interact with APP, and due its
 CC interaction with presenilins and KIAA0427 it is likely to play a major
 CC role in the pathogenesis of Alzheimer's disease. APP metabolism is also a
 CC critical event in Alzheimer's disease pathogenesis as it leads to the
 CC release of either toxic (Abeta) or trophic (sAPP) metabolites. Fe65 (not
 CC defined) has been shown to interact with APP and peptides interacting
 CC with Fe65 may also be useful in treating neurodegenerative disorders. The
 CC compound may be capable of strengthening the interaction between the first
 CC and the second protein. The sequence presented is the human PN7740
 CC protein which was isolated due to its interaction with Fe65 found using
 CC the yeast two-hybrid system
 XX
 XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
 QY 61 WDNFGIWDNRIDEPILLPSPKIPKISLENVGCASQIGKRKENEDEFDFQAULTDEV 120
 Db 61 WDNFGIWDNRIDEPILLPSPKIPKISLENVGCASQIGKRKENEDEFDFQAULTDEV 120
 QY 121 LYFAVDGHHGGAADFCCHTHMEKIMDLKPKEKNLETLTLTFLAFLDKAFSSHARLSAD 180
 Db 121 LYFAVDGHHGGAADFCCHTHMEKIMDLKPKEKNLETLTLTFLAFLDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAVNSLGQPHVNGRLANTRISIGDLTKTSGVIAPETPKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAVNSLGQPHVNGRLANTRISIGDLTKTSGVIAPETPKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
 DB 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
 QY 361 FSRSPASSGRWA 372
 DB 361 FSRSPASSGRWA 372

RESULT 6 ABG70826

ID ABG70826 standard; protein; 372 AA.

XX AC ABG70826;

DI 17-DEC-2002 (first entry)

DE Fe65 interacting human protein, PN7740, protein.

XX Yeast two-hybrid; PN7740; human; CIB; calcium-binding protein; MLK2;
 KW mixed lineage kinase 2; ligand; transporter; cellular uptake;
 KW neuronal death; neurodegenerative disorder; Huntington's disease;
 KW Parkinson's disease; dementia; Alzheimer's disease; APP; presenilin; PS1;
 KW PS2; Abeta; trophic; sAPP; metabolite; Fe65.

XX Homo sapiens.

XX US2002119155-A1.

XX 29-AUG-2002.

XX 09-OCT-2001; 2001US-00972038.

XX 17-OCT-2000; 2000US-0240790P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Roch J, Bartel PL, Heichman K;

XX WPI; 2002-750045/81.

XX N-PSDB; ABS55238.

XX Novel protein complex useful for screening for drug that modulates
 interaction of the proteins, has two proteins chosen from a complex of
 CIB or its fragment, and mixed lineage kinase 2 or its fragment.

XX Example 6; Page 22; 36pp; English.

XX The invention discloses an isolated protein complex comprising two
 proteins, chosen from a complex of CIB (calcium-binding protein), or its
 fragment, and mixed lineage kinase 2 (MLK2), or its fragment. The complex
 is useful for diagnosing a neurodegenerative disorder in an animal, by
 assaying whether the protein complex is present in a tissue extract, the
 ability of proteins to form the complex and a mutation in a gene encoding
 a protein of the complex and for determining whether a mutation in a gene
 encoding one of the proteins of the complex is useful for diagnosing a
 neurodegenerative disorder, where the inability to form the complex is
 indicative of the mutation. The complex is also useful for diagnosing
 (predisposition or existence of) neurodegenerative disorders such as
 Huntington's disease, Parkinson's disease, dementia and Alzheimer's
 disease, in humans, for screening for drug candidates that are capable of
 modulating the interaction of the first and second proteins, for the
 generation of antibodies, for the identification of agents that are
 capable of modulating the interactions, which are useful for treating the
 above mentioned neurodegenerative disorders and for screening individuals
 who are at risk of developing neurodegenerative disorders. The technique
 used to discover additional proteins that interact with the major
 Alzheimer's disease proteins (including APP, not defined, and

CC presenilins) was the yeast two-hybrid system. CIB has been shown to
 interact with the presenilins, PS1 and PS2, but due to the casual role of
 mutations of these presenilins in Alzheimer's disease, other proteins,
 CC like MLK2, are likely to play a major role in the pathogenesis. APP
 CC metabolism is also a critical event in Alzheimer's disease pathogenesis
 CC as it leads to the release of either toxic (Abeta) or trophic (sAPP)
 CC metabolites. Fe65 (not defined) has been shown to interact with APP and
 CC peptides interacting with Fe65 may also be useful in treating
 CC neurodegenerative disorders. The sequence presented is the human PN7740
 CC protein which was isolated due to its interaction with Fe65 found using
 CC the yeast two-hybrid system

XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLQLDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
 DB 1 MSTAALITLVRSQGNQVRRVLLSRLQLDDRRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
 QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLNVGCSAQIGKRKENEDRFPDQJLTDEV 120
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLNVGCSAQIGKRKENEDRFPDQJLTDEV 120
 QY 121 LYPVVDYDGHGGAADFCCHTHMEKICIMDLPPKXNLETLTLTAFLEIDKAFSSHARLSAD 180
 DB 121 LYPVVDYDGHGGAADFCCHTHMEKICIMDLPPKXNLETLTLTAFLEIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSEKILCRKGKPKMLTIDHTPERKDEKERIKK 240
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDSEKILCRKGKPKMLTIDHTPERKDEKERIKK 240
 QY 241 GGFVAVNSLGQPHVNGRLANTRISIGDLTKTSGVIAEPTPKIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAVNSLGQPHVNGRLANTRISIGDLTKTSGVIAEPTPKIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
 DB 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQYGTEDNSTAVVPPFGAWGKYKNSSEINFS 360
 QY 361 FSRSPASSGRWA 372
 DB 361 FSRSPASSGRWA 372

RESULT 7 ABB07402

ID ABB07402 standard; protein; 372 AA.

XX AC ABB07402;

XX 09-APR-2002 (first entry)

XX Human protein phosphatase IIC AB12 polypeptide.

XX Protein phosphatase IIC AB12; antiasthmatic; antiapoptotic; anti-HIV;
 KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
 KW antiinflammatory; anabolic; cancer.

XX Homo sapiens.

XX WC2001196571-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-BF006666.

XX 16-JUN-2000; 2000US-0212043P.

XX 07-AUG-2000; 2000US-0223322P.

XX 13-DEC-2000; 2000US-0254877P.

PA (FARB) BAYER AG.
 PI Xiao Y;
 XX WPI; 2002-139713/18.
 XX
 XX Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX
 XX Claim 26; Fig 19; 135pp; English.
 XX
 XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide
 XX
 XX Sequence 372 AA;
 SQ

Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGNVRRLVSSRLQLDDRRVPTCHSSTSEPCSRFPDGGSPAT 60
 DB 1 MSTAALITLVRSNGNVRRLVSSRLQLDDRRVPTCHSSTSEPCSRFPDGGSPAT 60
 QY 61 WDNFGIWNDRIDEPIILPPSIKYGKPIPKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 DB 61 WDNFGIWNDRIDEPIILPPSIKYGKPIPKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 QY 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLFIDKAFSSHARLSAD 180
 DB 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLFIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLQOPHYNGRLAMTRISIGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAMNSLQOPHYNGRLAMTRISIGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHTEQAIQYGTEDNSTAVVVPFGANGKYKNSFINEPS 360
 DB 301 NFVNSQIEICDFVNOCHDPNEAAHVAHTEQAIQYGTEDNSTAVVVPFGANGKYKNSFINEPS 360
 QY 361 FRSFASSGRWA 372
 DB 361 FRSFASSGRWA 372

RESULT 8
 AAE23976
 ID AAE23976 standard; protein; 372 AA.
 XX
 AC AAE23976;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Human PN7740 protein.

XX Human; protein-protein interaction; neurodegenerative disorder;
 KW Alzheimer's disease; AD; pharmaceutical; Huntington's disease;
 KW Parkinson's disease; anticonvulsant; dementia; neuroprotective;
 KW nootropic; PN7740.
 XX
 OS Homo sapiens.
 PN WO200233113-A2.
 XX
 XX 25-APR-2002.
 XX
 XX 16-OCT-2001; 2001WO-US032197.
 XX
 XX 17-OCT-2000; 2000US-0240790P.
 XX (MYRI-) MYRIAD GENETICS INC.
 XX
 XX Roch J, Bartel PL, Heichman K;
 WPI; 2002-454608/48.
 N-PSDB; AAD38691.
 XX
 XX New protein complex comprising Mint2 and PDE-9A proteins, useful as
 PT targets for diagnostic tools in identifying individuals at risk for
 PT neurodegenerative disorders, e.g. Alzheimer's disease, Parkinson's
 PT disease, or dementia.
 XX
 XX Example 6; Page 52; 91pp; English.
 XX
 XX The invention relates to the discovery of protein-protein interactions
 CC that are involved in the pathogenesis of neurodegenerative disorders,
 CC including Alzheimer's disease (AD). The AD interacting proteins are
 CC useful as new targets for the identification of useful pharmaceuticals,
 CC new targets for diagnostic tools in the identification of individuals at
 CC risk, sequences for producing transformed cell lines, cellular models and
 CC animal models, and new bases for therapeutic intervention in
 CC neurodegenerative disorders, particularly AD. The DNA encoding the
 CC protein of the invention can be used to create animals that overexpress
 CC the protein, or animals which do not express the native gene but express
 CC the protein. Modulators of the protein complex are useful for treating a
 CC neurodegenerative disorder including Huntington's disease, Parkinson's
 CC disease, dementia or Alzheimer's disease. The present sequence is human
 CC PN7740 protein used in the exemplification of the invention
 XX
 XX Sequence 372 AA;
 SQ

Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. NO. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGNVRRLVSSRLQLDDRRVPTCHSSTSEPCSRFPDGGSPAT 60
 DB 1 MSTAALITLVRSNGNVRRLVSSRLQLDDRRVPTCHSSTSEPCSRFPDGGSPAT 60
 QY 61 WDNFGIWNDRIDEPIILPPSIKYGKPIPKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 DB 61 WDNFGIWNDRIDEPIILPPSIKYGKPIPKISLENVGCASQIGKRKENEFRDFAQLTDEV 120
 QY 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLFIDKAFSSHARLSAD 180
 DB 121 LYFAVYDGHGGPAAADFCHTHMEKCIIMDLKPKEKNLETLTLTAFLFIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSPAILCRKKGPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLQOPHYNGRLAMTRISIGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAMNSLQOPHYNGRLAMTRISIGDLDLKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFVNSQIEICDFVNOCHDPNEAAHVAHTEQAIQYGTEDNSTAVVVPFGANGKYKNSFINEPS 360
 DB 301 NFVNSQIEICDFVNOCHDPNEAAHVAHTEQAIQYGTEDNSTAVVVPFGANGKYKNSFINEPS 360

Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIYQGTEDNSTAVVVPFGAWGKYKNSINFS 360
 Qy 361 FSRSPASSGRWA 372
 Db 361 FSRSPASSGRWA 372

RESULT 9
 AAE24078
 ID AAE24078 standard; protein; 372 AA.
 XX
 AC AAE24078;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human PN7740 protein.
 XX
 KW Protein complex; postsynaptic density protein; PSD95; Fe65; dementia;
 KW neurodegenerative disorder; Huntington's disease; Parkinson's disease;
 KW PN7740; Alzheimer's disease; drug designing; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200232286-A2.
 XX
 PD 25-APR-2002.
 XX
 PF 16-OCT-2001; 2001WO-US032186.
 XX
 PR 17-OCT-2000; 2000US-0240790P.
 PR 13-JUL-2001; 2001US-0304775P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Roch J, Bartel PL, Heichman K;
 XX
 DR WPI; 2002-479640/51.
 DR N-PSDB; AAD39176.
 XX
 PT Novel isolated protein complex having a protein which is postsynaptic
 PT density protein or Fe65 interacting with another protein which is PN7740
 PT useful for drug designing for treating neurodegenerative disorder.
 XX
 PS Claim 24; Page 52; 102pp; English.
 XX
 CC The invention relates to an isolated protein complex having a first
 CC protein which is postsynaptic density protein (PSD95) or Fe65 interacting
 CC with a second protein which is PN7740. Protein complex of the invention
 CC is useful for diagnosing a neurodegenerative disorder in human, for
 CC determining a predisposition to the neuro- degenerative disorder or for
 CC the existence of the disorder. They are used for treating degenerative
 CC disorders such as Huntington's disease, Parkinson's disease, dementia and
 CC Alzheimer's disease. They are also used for drug designing and for
 CC screening compounds that modulate the interaction of proteins of the
 CC invention. The present sequence is human PN7740 protein
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALTLVRSNGNVRRLVLSRLLODDRRVPTCHSSTSPRCRDPDGGSGSPAT 60
 Db 1 MSTAALTLVRSNGNVRRLVLSRLLODDRRVPTCHSSTSPRCRDPDGGSGSPAT 60
 Qy 61 WDNFGIWNDRIDEPTLLPPSKYKPIKISLENVGCSAQIGKKEKEDRDFEAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPTLLPPSKYKPIKISLENVGCSAQIGKKEKEDRDFEAQLTDEV 120
 Qy 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLDPKKNLETLTLTFLAFLDKAFSSHARLSAD 180
 Db 121 LYFAVYDGHGGPAAADFCFTHMEKICIMDLDPKKNLETLTLTFLAFLDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVWASVGSRAILCLCKGKPMKLTIDHTPERKDEKERIKK 240
 Db 181 ATLLTSGTTATVALLRDGIELVWASVGSRAILCLCKGKPMKLTIDHTPERKDEKERIKK 240
 Qy 241 GGFVAVNSLQOPHVNGRLAMTRESIGDLTKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 Db 241 GGFVAVNSLQOPHVNGRLAMTRESIGDLTKTSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
 Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIYQGTEDNSTAVVVPFGAWGKYKNSINFS 360
 Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIYQGTEDNSTAVVVPFGAWGKYKNSINFS 360
 Qy 361 FSRSPASSGRWA 372
 Db 361 FSRSPASSGRWA 372

RESULT 10
 AAE14451
 ID AAE14451 standard; protein; 372 AA.
 XX
 AC AAE14451;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human protein phosphatase-1.
 XX
 KW Human; protein phosphatase; PP-1; immune system disorder; AIDS; allergy;
 KW neurological disorder; developmental disorder; Alzheimer's disease;
 KW cell proliferative disorder; Huntington's disease; arteriosclerosis;
 KW renal tubular acidosis; gonadal dysgenesis; cancer; adenocarcinoma;
 KW leukaemia; transgenic animal; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 104..339
 FT /note= "Protein phosphatase 2C (Pp2C) "
 FT Domain 122..130
 FT /label= Protein_phosphatase_2C_motif
 XX
 PN WO200196546-A2.
 XX
 PD 20-DEC-2001.
 XX
 PF 14-JUN-2001; 2001WO-US019442.
 XX
 PR 16-JUN-2000; 2000US-0212447P.
 PR 22-JUN-2000; 2000US-0213746P.
 PR 29-JUN-2000; 2000US-0215210P.
 PR 06-JUL-2000; 2000US-0215299P.
 PR 12-JUL-2000; 2000US-0218080P.
 PR 21-JUL-2000; 2000US-0220117P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Au-Yeung J, Baughn MR, Ding L, Elliott VS, Gandhi AR, Griffin JA;
 PI Hafalia A, Kearney L, Lee EA, Lu Y, Nguyen DB, Patterson C;
 PI Ramkumar J, Reddy R, Sanjanwala MS, Stewart EA, Tang YT, Thornton M;
 PI Tribouley CM, Wallia NK, Yang J, Yao MG, Yue H;
 XX
 DR WPI; 2002-090206/12.
 DR N-PSDB; AAD24019.
 XX
 PT Novel polypeptide, useful for diagnosing, treating or preventing
 PT disorders of growth and development, immune system, neurological and cell
 PT proliferation diseases, comprises cancer protein phosphatase
 PT polypeptides.
 XX
 PS Claim 1; Page 102-103; 116pp; English.
 XX
 CC The present sequence is human protein phosphatase (PP)-1. PP

CC polynucleotide and polypeptide are useful in the diagnosis, treatment and
 CC prevention of immune system disorders, neurological disorders,
 CC developmental disorders and cell proliferative disorders. Examples of
 CC immune system disorders include acquired immune deficiency syndrome
 CC (AIDS), severe combined immunodeficiency disease (SCID), adult
 CC respiratory distress syndrome, allergies, amyloidosis, anaemia, asthma,
 CC atherosclerosis, Crohn's disease, atopic dermatitis, diabetes mellitus,
 CC emphysema, Goodpasture's syndrome, gout, Graves' disease, multiple
 CC sclerosis, myasthenia gravis, myocardial or pericardial inflammation,
 CC osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
 CC rheumatoid arthritis, Sjogren's syndrome, scleroderma, systemic
 CC sclerosis, trauma, neurological disorders include Alzheimer's disease,
 CC Huntington's disease, dementia, epilepsy, Parkinson's disease, mental
 CC retardation and other developmental disorders of central nervous system
 CC such as Down's syndrome, cerebral palsy, periodic paralysis, mental
 CC disorders including mood, anxiety, and schizophrenic disorders, seasonal
 CC affective disorder such as akathisia, amnesia, catatonia, dyskinesia;
 CC developmental disorders include e.g. renal tubular acidosis, Duchenne and
 CC Becker muscular dystrophy, gonadal dysgenesis, hypothyroidism; cell
 CC proliferative disorders include e.g. actinic keratosis, arteriosclerosis,
 CC atherosclerosis, bursitis, cirrhosis, hepatitis, psoriasis and cancer
 CC including adenocarcinoma, leukaemia. The polypeptide and polynucleotide
 CC are further useful for analysing proteome of a tissue or a cell type, for
 CC screening an agonist/antagonist, a compound that specifically binds to it
 CC or its modulator. The polynucleotide is useful for creating knockin
 CC humanised animals (pigs) or transgenic animals (mice or rats) to model
 CC human disease, for generating a transcript image of a tissue or cell
 CC type, which represents the global pattern of gene expression by a
 CC particular tissue or cell type
 CC
 XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 5; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSRFPDGGSPAT 60
 DB 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSRFPDGGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRKENEDRFDFAQLTDEV 120
 DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRKENEDRFDFAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCHTHMEKIMDLPLPEKXLETLTLTAFLEIDKATSSSHARLSAD 180
 DB 121 LYFAVVDGHHGGAADFCHTHMEKIMDLPLPEKXLETLTLTAFLEIDKATSSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDGRAILCRKGPMLTIDHTPERKDEKERIKKC 240
 DB 181 ATLLTSGTTATVALLRDGIELVVASVGDGRAILCRKGPMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVANSIGQPHVNGRLAWTSIGDLDTKSGVTAEPETKRIKLHHADDSFLVLTDDGI 300
 DB 241 GGFVANSIGQPHVNGRLAWTSIGDLDTKSGVTAEPETKRIKLHHADDSFLVLTDDGI 300

QY 301 NFVNSQIECDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVPFGWAGKYKSEINFS 360
 DB 301 NFVNSQIECDFVNOCHDNEAAHVAETQAIQYGTEDNSTAVVPFGWAGKYKSEINFS 360

QY 361 FRSFASGRWA 372
 DB 361 FRSFASGRWA 372

RESULT 11
 ABU10309
 ID ABU10309 standard; protein; 372 AA.

XX ABU10309;

AC ABU10309;

XX 07-AUG-2003 (first entry)

XX

DE Human protein phosphatase SGP037.
 XX Human; protein phosphatase; SGP037; cancer; blood; haematopoietic;
 KW breast; colon; lung; prostate; cervical; brain; ovarian; bladder; kidney;
 KW immune-related disease; cardiovascular disease; migraine;
 KW neuronal-associated disease; nervous system disease; pain; rhinitis;
 KW sexual dysfunction; mood disorder; attention disorder; hypotension;
 KW cognition disorder; hypertension; psychotic disorder; dyskinesia;
 KW neurological disorder; metabolic disorder; inflammatory disorder;
 KW rheumatoid arthritis; chronic inflammatory bowel disease; asthma;
 KW chronic inflammatory pelvic disease; multiple sclerosis; psoriasis;
 KW osteoarthritis; psoriasis; atherosclerosis; autoimmunity; nocropic;
 KW organ transplant rejection; cytostatic; neuroprotective; analgesic;
 KW hypotensive; anticonvulsant; antiarthritic; antirheumatic;
 KW antiinflammatory; antisthmatic; osteopathic; antipsoriatic;
 KW antiarteriosclerotic; immunosuppressive; enzyme.

OS Homo sapiens.

XX US2003027308-A1.

XX 06-FEB-2003.

XX 13-NOV-2001; 2001US-00986992.

XX 30-MAY-2000; 2000US-0208291P.

XX 13-NOV-2000; 2000US-0246974P.

XX (SUGE-) SUGEN INC.

XX Plowman GD, Whyte D, Manning G;

XX WPI; 2003-466146/44.

XX N-PSDB; ABX95873.

XX New isolated, enriched or purified nucleic acid molecule encoding a
 PT phosphatase polypeptide, useful for treating diseases, e.g. cancers, or
 PT immune-related, cardiovascular, brain and neuronal, metabolic or
 PT inflammatory disorders.

XX Claim 1; Fig 2; 45pp; English.

XX The present invention relates to the isolation of a novel human protein
 CC phosphatase designated SGP037, and the polynucleotide sequence encoding
 CC it. The gene encoding human SGP037 maps to chromosome 4q21. The SGP037
 CC polypeptide and the polynucleotide sequence encoding it are useful for
 CC treating diseases or disorders such as cancers (e.g. cancer of the blood
 CC or haematopoietic origin, breast, colon, lung, prostate, cervical, brain,
 CC ovarian, bladder or kidney), immune-related diseases and disorders,
 CC cardiovascular diseases, brain and neuronal-associated diseases (e.g.
 CC central or peripheral nervous system diseases, migraines, pain, sexual
 CC dysfunction, mood disorders, attention disorders, cognition disorders,
 CC dyskinesias), metabolic disorders, and inflammatory disorders (e.g.
 CC rheumatoid arthritis, chronic inflammatory bowel disease, chronic
 CC inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis,
 CC psoriasis, atherosclerosis, rhinitis, autoimmunity or organ transplant
 CC rejection). The present sequence represents human SGP037

XX Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 6; Length 372;

Best Local Similarity 100.0%; Pred. No. 1.5e-206;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSRFPDGGSPAT 60

DB 1 MSTAALITLVRSQGNQVRRVLLSRLLQDDRRVPTCHSSTSEPCRSRFPDGGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRKENEDRFDFAQLTDEV 120

DB 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLVNVCASQIGKRKENEDRFDFAQLTDEV 120

QY 121 LYFAVYDGHGGPAAADFCHTHMEKIMDILLPKEKNLETLTLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGPAAADFCHTHMEKIMDILLPKEKNLETLTLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSGVIAPEPKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSGVIAPEPKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 360
QY 361 FSRSPASSGRWA 372
DB 361 FSRSPASSGRWA 372

RESULT 12
AAO23055
ID AAO23055 standard; protein; 372 AA.
AC AAO23055;
DT 17-SEP-2003 (first entry)
XX Human serine/threonine PP2C phosphatase SGP037 protein.
KW Cytostatic; immunosuppressive; cardiovascular; hypotensive; hypertensive;
KW antimigraine; analgesic; nootropic; tranquiliser; antirheumatic; brain;
KW antiarthritic; antiinflammatory; gynaecological; neuroprotective; ocular;
KW antiasthmatic; osteopathic; antipsoriatic; antiarteriosclerotic; obesity;
KW antiallergic; serine threonine phosphatase; STP; PP2C; cancer; immune;
KW cardiovascular disease; neuronal; sexual dysfunction; migraine; glaucoma;
KW psychotic; neurological; schizophrenia; metabolic; inflammatory; SGP037;
KW multiple sclerosis; viral infection; HIV; transgenic; gene therapy;
KW enzyme; human; chromosome 4q21.
XX
OS Homo sapiens.
XX
FH Key
FT Region
FT 104..339
XX /note= "Catalytic region"
PN WO2003042390-A1.
XX
PD 22-MAY-2003.
XX
PF 13-NOV-2001; 2001WO-US043063.
XX
PR 13-NOV-2001; 2001WO-US043063.
XX
PA (PLOW/) PLOWMAN G D.
PI Plowman GD, Manning G, Whyte D;
XX
DR WPI; 2003-449576/42.
DR N-PSDB; AAL55773.
XX
PT New phosphatase nucleic acid molecule and polypeptide, useful for
PT diagnosing or treating phosphates-related disorders such as cancers,
PT immune-related disorders, cardiovascular disease, and inflammatory
PT disorders.
XX
PS Claim 26; Fig 2; 152pp; English.
XX
CC The invention relates to a novel isolated nucleic acid molecule encoding
CC a serine/threonine phosphatase (STP) polypeptide which is a member of the
CC PP2C family. PP2C phosphatases are involved in a number of cellular
CC processes including modulation of integrin signal transduction and

CC regulation of the TAK1 signalling pathway, cellular channels, cyclin
CC dependent kinases and the Ras pathway. The methods and compositions of
CC the present invention may be useful during the diagnosis or treatment of
CC a variety of disorders including cancers, immune-related and
CC cardiovascular disease, brain or neuronal-associated diseases such as
CC sexual dysfunction and migraine, psychotic and neurological disorders
CC e.g. schizophrenia and metabolic disorders such as obesity. Furthermore,
CC ocular disease, such as glaucoma and inflammatory disorders e.g. multiple
CC sclerosis may be addressed, as well as viral infections caused by HIV and
CC other pathological agents. Finally, the molecules of the invention may be
CC utilised in the production of transgenic animals and during gene therapy.
CC The current sequence is that of the human serine/threonine PP2C
CC phosphatase SGP037 protein of the invention
XX
SQ Sequence 372 AA;

Query Match 100.0%; Score 1951; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e-206;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSPAT 60
DB 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPESIKYGRPIPKISLENVGCASQICKRKENEDRFPQALTDEV 120
DB 61 WDNFGIWDNRIDEPILLPESIKYGRPIPKISLENVGCASQICKRKENEDRFPQALTDEV 120
QY 121 LYFAVYDGHGGPAAADFCHTHMEKIMDILLPKEKNLETLTLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVYDGHGGPAAADFCHTHMEKIMDILLPKEKNLETLTLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDSSRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSGVIAPEPKRIKLHHADDSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSGDLDLKTSGVIAPEPKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 360
QY 361 FSRSPASSGRWA 372
DB 361 FSRSPASSGRWA 372

RESULT 13
ADB66824
ID ADB66824 standard; protein; 372 AA.
XX
AC ADB66824;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human PN7740.
XX
KW human; drug candidate screening; neurodegenerative disorder;
KW Huntington's disease; Parkinson's disease; dementia; Alzheimer's disease.
XX Homo sapiens.
OS
XX US2002115119-A1.
PN
XX 22-AUG-2002.
PD
XX 10-OCT-2001; 2001US-00973063.
PF
XX 17-OCT-2000; 2000US-0240790P.
PR
XX (MYRI-) MYRIAD GENETICS INC.
PA

XX PI Roch J, Bartel PL, Heichman K;
 XX WPI; 2003-719962/68.
 XX N-PSDB; ADB66827.
 XX Screening drug candidates for modulating interaction of complexes of
 PT protein, by combining protein in the presence or absence of a drug to
 PT form first and second complex, and measuring and comparing both the
 XX complexes.
 XX Example 2; Page 22; 36pp; English.
 XX The invention relates to a method of screening drug candidates for
 CC modulating interaction of proteins in a complex. The method is useful for
 CC screening drug candidates useful in treating neurodegenerative disorder,
 CC by measuring the activity of a protein selected from Mint2 and PDE-9A in
 CC the presence or absence of the drug, and comparing the activity measured,
 CC where if there is a difference in activity, then the drug is a drug
 CC candidate for treating the neurodegenerative disorder. The
 CC neurodegenerative disorder is Huntington's disease. Parkinson's disease,
 CC dementia, or Alzheimer's disease, preferably Alzheimer's disease. The
 CC drug, modulator or compound identified by the methods of the invention
 CC are useful for treating a neurodegenerative disorder. The present
 CC sequence represents the amino acid sequence of human FN7740.
 XX
 XX Sequence 372 AA;
 SQ
 Query Match 100.0%; Score 1951; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSQGNVRRVLLSSRLLODDRVTPTCHSSTSEPCRSRFPDPGSGSPAT 60
 DB 1 MSTAALITLVRSQGNVRRVLLSSRLLODDRVTPTCHSSTSEPCRSRFPDPGSGSPAT 60
 QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFPAQLTDEV 120
 DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFPAQLTDEV 120
 QY 121 LYFAVYDGHGGAADPCHTHMEKCIIMDLKPKNLETLTLAFLIDKAFSSHARLSAD 180
 DB 121 LYFAVYDGHGGAADPCHTHMEKCIIMDLKPKNLETLTLAFLIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
 QY 241 GGFVAMNSLQOPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAMNSLQOPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQEICDFVNOCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINF 360
 DB 301 NFMVNSQEICDFVNOCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINF 360
 QY 361 FSRSPASSGRWA 372
 DB 361 FSRSPASSGRWA 372
 RESULT 14
 ADD73452
 ID ADD73452 standard; protein; 372 AA.
 XX
 AC ADD73452;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel human protein FN7740.
 XX
 KW nootropic; neuroprotective; antiparkinsonian; protein binding modulator;
 KW drug screening; neurodegenerative disorder; Huntington's Disease;

KW Parkinson's Disease; dementia; Alzheimer's Disease; AD; APP; presenilin;
 KW protein-protein interaction; drug target identification; human;
 XX yeast two-hybrid assay; PN7740.
 XX Homo sapiens.
 XX US2003186317-A1.
 XX 02-OCT-2003.
 XX 09-OCT-2001; 2001US-00971782.
 XX 17-OCT-2000; 2000US-024079CP.
 XX (MYRI-) MYRIAD GENETICS INC.
 XX Roch J, Bartel PL, Heichman K;
 XX WPI; 2003-852417/79.
 XX N-PSDB; ADB73455.
 XX In vitro screening for drug useful for treating neurodegenerative
 PT disorder, e.g. Alzheimer's Disease, involves comparing the amount of two
 PT complexes formed from combined proteins of protein complex in the
 PT presence and absence of drug.
 XX Example 2-33; SEQ ID NO 4; 36pp; English.
 CC The invention describes screening a drug in vitro by combining proteins
 CC of a protein complex in the presence of a drug to form a first complex;
 CC combining the proteins in the absence of the drug to form a second
 CC complex; measuring the amount of the two complexes; and comparing the
 CC amount of the first complex with the amount of the second complex. The
 CC method is useful for screening drug candidates capable of modulating a
 CC interaction of the proteins of a protein complex, useful for treating a
 CC neurodegenerative disorder, e.g. Huntington's Disease, Parkinson's
 CC Disease, dementia or Alzheimer's Disease (AD). The inventive method
 CC provides for the discovery of additional proteins interacting with
 CC various domains of the major Alzheimer proteins, including APP and the
 CC presenilins. It can also identify the protein-protein interactions that
 CC are involved in Alzheimer's Disease (AD) pathogenesis, and to identify
 CC drug targets. This is the amino acid sequence of a novel human protein
 CC PN7740 identified using yeast two-hybrid assay with a human brain bait
 CC protein.
 XX
 SQ Sequence 372 AA;
 Query Match 100.0%; Score 1951; DB 7; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.5e-206;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSQGNVRRVLLSSRLLODDRVTPTCHSSTSEPCRSRFPDPGSGSPAT 60
 DB 1 MSTAALITLVRSQGNVRRVLLSSRLLODDRVTPTCHSSTSEPCRSRFPDPGSGSPAT 60
 QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFPAQLTDEV 120
 DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGKRKENEPRDFPAQLTDEV 120
 QY 121 LYFAVYDGHGGAADPCHTHMEKCIIMDLKPKNLETLTLAFLIDKAFSSHARLSAD 180
 DB 121 LYFAVYDGHGGAADPCHTHMEKCIIMDLKPKNLETLTLAFLIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
 DB 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKK 240
 QY 241 GGFVAMNSLQOPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300
 DB 241 GGFVAMNSLQOPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQEICDFVNOCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINF 360
 DB 301 NFMVNSQEICDFVNOCHDNEAAHVAITEQAIOYGTEDNSTAVVVPFGAMGKYKNSSEINF 360

Db 301 NFMVNSQICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAWGKYKXNSEINFS 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 15
ADA54131
ID ADA54131 standard; protein; 372 AA.
AC ADA54131;
XX 20-NOV-2003 (first entry)
XX Human protein, SEQ ID 1699.
XX
XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
XX Homo sapiens.
XX
XX EPI293569-A2.
XX
XX 19-MAR-2003.
XX
XX 21-MAR-2002; 2002EP-00006586.
XX
XX 14-SEP-2001; 2001JP-00328381.
XX
XX 24-JAN-2002; 2002US-0350435P.
XX
XX (HELI-) HELIX RES INST.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI; 2003-395539/38.
XX
XX N-ESDB; ADA52492.
XX
XX New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
XX Claim 14; SEQ ID NO 1699; 205pp; English.
XX
XX The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
XX inflammatory diseases, osteoporosis or neurological disease.

Query Match 99.9%; Score 1950; DB 6; Length 372;
Best Local Similarity 99.7%; Pred. No. 2e-206;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGVRRVLLSRLLQDDRRVPTCHSSTSPRCRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGVRRVLLSRLLQDDRRVPTCHSSTSPRCRFPDGGSGSPAT 60
QY 61 WDNFGIWNRIDEPILLPPSIKYGPPIKISLVNVCASQIGKKNEDRDFDLTLDEV 120
Db 61 WDNFGIWNRIDEPILLPPSIKYGPPIKISLVNVCASQIGKKNEDRDFDLTLDEV 120
QY 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPPKKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGPAAADFCHTHMEKIMDLPPKKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLSGTATVALLRDGIELVWASVGSRAILCKGKPKMLTIDHTPERKDEKERIKKC 240

Db 181 ATLLSGTATVALLRDGIELVWASVGSRAILCKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAVNSILGQPHVNGRLAMTRSIGDLDLKTSGVIAEPETKRIKLHADDGFLVLTDDGI 300
Db 241 GGFVAVNSILGQPHVNGRLAMTRSIGDLDLKTSGVIAEPETKRIKLHADDGFLVLTDDGI 300
QY 301 NFMVNSQICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAWGKYKXNSEINFS 360
Db 301 NFMVNSQICDFVNOCHDPNEAAHVAETEQAIOYGTEDNSTAVVVPFGAWGKYKXNSEINFS 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 16
AAU22934
ID AAU22934 standard; protein; 373 AA.
XX AAU22934;
XX
XX 18-DEC-2001 (first entry)
XX
XX Novel human enzyme polypeptide #20.
XX
XX Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW ligase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; cytostatic; anti arthritic;
KW nephrotropic; anticoagulant.
XX
XX Homo sapiens.
XX
XX WO200155301-A2.
XX
XX 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US001239.
XX
XX 31-JAN-2000; 2000US-0179065P.
XX
XX 04-FEB-2000; 2000US-0180628P.
XX
XX 24-FEB-2000; 2000US-0184664P.
XX
XX 02-MAR-2000; 2000US-0186350P.
XX
XX 16-MAR-2000; 2000US-0189874P.
XX
XX 17-MAR-2000; 2000US-0190076P.
XX
XX 18-APR-2000; 2000US-0198123P.
XX
XX 19-MAY-2000; 2000US-0205515P.
XX
XX 07-JUN-2000; 2000US-0209467P.
XX
XX 28-JUN-2000; 2000US-0214886P.
XX
XX 30-JUN-2000; 2000US-0215135P.
XX
XX 07-JUL-2000; 2000US-0216647P.
XX
XX 07-JUL-2000; 2000US-0216880P.
XX
XX 11-JUL-2000; 2000US-0217487P.
XX
XX 14-JUL-2000; 2000US-0218290P.
XX
XX 26-JUL-2000; 2000US-0220963P.
XX
XX 26-JUL-2000; 2000US-0220964P.
XX
XX 14-AUG-2000; 2000US-0224518P.
XX
XX 14-AUG-2000; 2000US-0225213P.
XX
XX 14-AUG-2000; 2000US-0225214P.
XX
XX 14-AUG-2000; 2000US-0225266P.
XX
XX 14-AUG-2000; 2000US-0225267P.
XX
XX 14-AUG-2000; 2000US-0225268P.
XX
XX 14-AUG-2000; 2000US-0225270P.
XX
XX 14-AUG-2000; 2000US-0225447P.
XX
XX 14-AUG-2000; 2000US-0225757P.
XX
XX 14-AUG-2000; 2000US-0225758P.
XX
XX 14-AUG-2000; 2000US-0225759P.
XX
XX 18-AUG-2000; 2000US-0226279P.
XX
XX 22-AUG-2000; 2000US-0226681P.

PR 23-AUG-2000; 2000US-0226868P.
PR 23-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 05-SEP-2000; 2000US-0230437P.
PR 08-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234233P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234597P.
PR 25-SEP-2000; 2000US-0234598P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 05-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-465566/50.

N-PSDB; AAS40804.

Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.

Claim 11; SEQ ID NO 930; 1180pp; English.

The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polynucleotides of the invention can also be used in gene therapy. AAU22915-AAU23814 represent the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 373 AA;

Query Match 99.4%; Score 1939; DB 4; Length 373;

Best Local Similarity 99.5%; Pred. No. 3.3e-205;

Matches 370; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQRRVRLSSLLQDDRRVPTCHSSSTSEPCRSRFDPDGSGSPAT 60

Db 2 MSTAALITLVRSQGNQRRVRLSSLLQDDRRVPTCHSSSTSEPCRSRFDPDGSGSPAT 61

QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFFAQLTDEV 120
 Db 62 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFFAQLTDEV 121
 QY 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXNLETLLTFLAFLEIDKAFSSHARLSAD 180
 Db 122 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXNLETLLTFLAFLEIDKAFSSHARLSAD 181
 QY 181 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKRIKCC 240
 Db 182 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKRIKCC 241
 QY 241 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 300
 Db 242 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 301
 QY 301 NFWMNSQICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 360
 Db 302 NFWMNSQICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 361
 QY 361 FSRSPASSGRWA 372
 Db 362 FSRSPASSGRWA 373

RESULT 17

AAB57077
 ID AAB57077 standard; protein; 373 AA.

AC AAB57077;

XX 13-MAR-2001 (first entry)

DE Human prostate cancer antigen protein sequence SEQ ID NO:1655.

XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;
 KW neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular;
 KW vulnery; gastrointestinal; nephrotoxic; antineoplastic; gynaecological;
 KW antibacterial; gene therapy; neural; immune; reproductive; renal;
 KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;
 KW wound; infectious disease.

XX Homo sapiens.

XX WO200055174-A1.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US005988.

XX 12-MAR-1999; 99US-0124270P.

XX (HUMA-) HUMAN GENOME SCI INC.
 XX (ROSE/) ROSEN C A.

PI Rosen CA, Ruben SM;

XX WPI; 2000-587513/55.

DR N-ESDB; AAF16280.

PT Prostate cancer associated gene sequences, referred to as prostate cancer
 PT antigens, useful for treatment, prevention, and diagnosis of disorders
 PT such as prostate cancer.

PS Claim 11; Page 2113-2114; 2338pp; English.

XX AAF15866 to AAF16505 encode the human prostate cancer associated
 CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.
 CC The prostate cancer antigens can have neuroprotective, cytostatic,
 CC cardioactive, immunomodulatory, muscular, vulnery, gastrointestinal,
 CC nephrotoxic, antineoplastic, gynaecological and antibacterial activities,
 CC and can be used in gene therapy. The prostate cancer antigen

CC polynucleotides may be used for detection of prostate cancer, chromosome
 CC identification, as chromosome markers, and for numerous other diagnostic
 CC or research purposes. The prostate cancer antigens may be used to treat
 CC disorders such as neural, immune, muscular, reproductive,
 CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative
 CC disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
 CC AAB57303 represent sequences used in the exemplification of the present
 CC invention

XX SQ Sequence 373 AA;

Query Match 98.6%; Score 1924; DB 3; Length 373;

Best Local Similarity 98.9%; Pred. No. 1.5e-203;

Matches 368; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGGNQVRRVLLSSRLQLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 60
 Db 2 MSTAALITLVRSGGNQVRRVLLSSRLQLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 61
 QY 61 WNFQIWNDRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFFAQLTDEV 120
 Db 62 WNFQIWNDRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFFAQLTDEV 121
 QY 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXNLETLLTFLAFLEIDKAFSSHARLSAD 180
 Db 122 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKKXNLETLLTFLAFLEIDKAFSSHARLSAD 181
 QY 181 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKRIKCC 240
 Db 182 ATLLTSGTTATVALLRGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKRIKCC 241
 QY 241 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 300
 Db 242 GGFVAMNSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 301
 QY 301 NFWMNSQICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 360
 Db 302 NFWMNSQICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGANGKYKNSINF 361
 QY 361 FSRSPASSGRWA 372
 Db 362 FSRSPASSGRWA 373

RESULT 18

ABB07401
 ID ABB07401 standard; protein; 351 AA.

XX AC ABB07401;

XX 09-APR-2002 (first entry)

DE Human protein phosphatase IIC ABI2 polypeptide.

XX Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
 KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
 KW antiinflammatory; anabolic; cancer.

OS Homo sapiens.

XX WO200196571-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-BP006666.

XX 16-JUN-2000; 2000US-0212043P.

XX 07-AUG-2000; 2000US-0223322P.

XX 13-DEC-2000; 2000US-0254877P.

XX (FARB) BAYER AG.

XX Xiao Y;

XX WPI: 2002-139713/18.
 DR N-PSDB; ABA94576.
 XX
 XX Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX
 XX Claim 26; Fig 18; 135pp; English.
 PS
 XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide
 XX
 XX Sequence 351 AA;
 SQ
 Query Match 92.7%; Score 1809; DB 5; Length 351;
 Best Local Similarity 100.0%; Pred. No. 7.4e-191;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCFFPDGSGSPAT 60
 Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCFFPDGSGSPAT 60
 QY 61 WNFQGWDRIDEPILLPSIKYKPIPKISLVNVCASQIGKRNEDRDFDFAQLTDEV 120
 Db 61 WNFQGWDRIDEPILLPSIKYKPIPKISLVNVCASQIGKRNEDRDFDFAQLTDEV 120
 QY 121 LYPVAVDGHGGAAADFCHTMEKIMDILLPKENKLETLTLTAFLEIDKAFSSHARLSAD 180
 Db 121 LYPVAVDGHGGAAADFCHTMEKIMDILLPKENKLETLTLTAFLEIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGRPKMTIDHTPERKDEKRIKCC 240
 Db 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKGRPKMTIDHTPERKDEKRIKCC 240
 QY 241 GGFVANSIGQPHVNGRLAMTSIGDLTKTSGLVLAEPETKRIKLHHADDSFLVLTDDGI 300
 Db 241 GGFVANSIGQPHVNGRLAMTSIGDLTKTSGLVLAEPETKRIKLHHADDSFLVLTDDGI 300
 QY 301 NFVWNSQEICDFVNOCHDPNEAAHVAETQAIQYGTEDNSTAVVVPF 346
 Db 301 NFVWNSQEICDFVNOCHDPNEAAHVAETQAIQYGTEDNSTAVVVPF 346

RESULT 19

ABB78059

ID ABB78059 standard; protein; 352 AA.

XX

AC ABB78059;

XX

DT 05-NOV-2002 (first entry)

XX

DE Amino acid sequence of human 16105 polypeptide.

XX

KW Human; 16105; cancer; cellular proliferation disorder; brain cancer;

KW cellular differentiation disorder; breast cancer; lung cancer;

KW ovarian cancer; cardiovascular disorder; hypertension; atherosclerosis;

KW arrhythmia; heart failure; endothelial cell disorder; psoriasis;

KW Grave's disease; autoimmune disease; diabetes mellitus; Crohn's disease;

KW viral disease; pain; metabolic disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 26..26
 FT /note= "protein kinase C phosphorylation site"
 FT Modified-site 32..35
 FT /note= "cAMP/cGMP-dependent protein kinase
 FT phosphorylation site"
 FT Modified-site 41..44
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 48..51
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 56..61
 FT /note= "N-myristoylation site"
 FT Modified-site 65..70
 FT /note= "N-myristoylation site"
 FT Modified-site 80..82
 FT /note= "protein kinase C phosphorylation site"
 FT Modified-site 101..104
 FT /note= "amidation site"
 FT Domain 104..323
 FT /note= "protein phosphatase domain"
 FT Domain 122..130
 FT /note= "protein phosphatase 2C signature"
 FT Modified-site 130..135
 FT /note= "N-myristoylation site"
 FT Modified-site 140..143
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 187..192
 FT /note= "N-myristoylation site"
 FT Modified-site 205..208
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 241..246
 FT /note= "N-myristoylation site"
 FT Modified-site 263..266
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 280..282
 FT /note= "protein kinase C phosphorylation site"
 FT Modified-site 338..341
 FT /note= "casein kinase II phosphorylation site"
 FT Modified-site 338..340
 FT /note= "protein kinase C phosphorylation site"
 XX
 XX US2002077463-A1.
 XX
 XX 20-JUN-2002.
 XX
 XX 17-MAY-2001; 2001US-00860351.
 XX
 XX 19-MAY-2000; 2000US-0205260P.
 XX
 XX (MEYE/) MEYERS R.
 XX Meyers R;
 XX WPI: 2002-607448/65.
 XX N-PSDB; ABO78296.
 XX
 XX New polypeptide for treating a subject having a disorder or at risk of
 XX developing a proliferative disorder, cardiovascular disorder, autoimmune
 XX or metabolic disorder.
 XX
 XX Claim 4; Fig 1a-b; 50pp; English.
 PS
 XX The present sequence represents a human polypeptide, designated 16105.
 CC 16105 polypeptides and polynucleotides are used for evaluating the
 CC efficacy of a treatment of cancer or a cellular proliferation and/or
 CC differentiation disorder in a subject. They are also useful for
 CC diagnosing a cancer or a cellular proliferation and/or differentiation
 CC disorder in a subject. The cancer or cellular proliferation and/or
 CC differentiation is breast, lung, brain or ovarian cancer. They may also

CC be used for treating proliferative disorders e.g., cancer; cardiovascular
CC disorders e.g., hypertension, atherosclerosis, arrhythmias, heart failure
CC ; endothelial cell disorders e.g., psoriasis, Grave's disease; autoimmune
CC diseases e.g., diabetes mellitus, Crohn's disease; viral diseases; pain;
CC or metabolic disorders
XX
SQ Sequence 352 AA;

Query Match 88.5%; Score 1727; DB 5; Length 352;
Best Local Similarity 99.4%; Pred. No. 8.9e-182;
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTAAALITLVRSQGNQVRRVLLSSRLQLDDRRVPTTCHSTSEPRCSRFPDGGSPAT 60
DB 1 MSTAAALITLVRSQGNQVRRVLLSSRLQLDDRRVPTTCHSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLVNVCASQIGKRKENEDRFPDQAULTDEV 120
DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLVNVCASQIGKRKENEDRFPDQAULTDEV 120
QY 121 LYFVAVYDGHGGPAAADFCHTHMEKIMDLPLKPKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
DB 121 LYFVAVYDGHGGPAAADFCHTHMEKIMDLPLKPKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVITDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVITDGI 300
QY 301 NFMVNSQEICDFVNQCHDPNEAAHVAETEQAIIQ 332
DB 301 NFMVNSQEICDFVNQCHDPNEAAHVAETEQAIIQ 332

RESULT 20

AD31687
ID ADE31687 standard; protein; 352 AA.
XX ADE31687;
AC ADE31687;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human 16105 protein #SEQ ID 44.
XX
KW Antiatherosclerotic; cardiac; vasotropic; antiinflammatory;
KW thrombolytic; antiarrhythmic; antianginal; hypotensive; gene therapy;
KW cardiovascular; disorder; ischaemia; aortic bending;
KW vascular heart disease; endocarditis; atrial fibrillation; heart failure;
KW angina; cardiomyopathy; cardiac death.
XX
OS Homo sapiens.
XX
PN WO2003065984-A2.
XX
ED 14-AUG-2003.
XX
FF 29-JAN-2003; 2003WO-US002571.
XX
PR 01-FEB-2002; 2002US-0353224P.
PR 15-MAR-2002; 2002US-0364529P.
PR 19-APR-2002; 2002US-0373861P.
PR 29-APR-2002; 2002US-0376287P.
PR 12-JUN-2002; 2002US-0388080P.
PR 24-JUN-2002; 2002US-0390971P.
PR 03-JUL-2002; 2002US-0394130P.
PR 10-JUL-2002; 2002US-0394797P.
PR 21-AUG-2002; 2002US-0404904P.
PR 23-AUG-2002; 2002US-0405450P.
PR 04-SEP-2002; 2002US-0408070P.
PR 06-NOV-2002; 2002US-0424300P.

PR 05-DEC-2002; 2002US-0431042P.
PR 05-DEC-2002; 2002US-0431079P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
PI Logan TJ, Chun M, Galvin KM, Healy A, Acton SL, Donaghue M;
PI Stagliano N, Perodin J, Rodrigue-Way A;
XX
XX WPI; 2003-731468/69.
DR N-PDDB; ADE31686.

Identifying a compound capable of treating a cardiovascular disorder
(e.g. atherosclerosis) comprises assaying the ability of the compound to
modulate the expression or activity of e.g. 1682, 6169 or 6193
polypeptide or nucleic acid.

PS Disclosure; SEQ ID NO 44; 328pp; English.

CC The invention relates to a method for identifying a compound capable of
CC treating a cardiovascular disorder. The present invention identifies the
CC differential expression of 1682, 6169, 6193, 7771, 14395, 29002, 33216,
CC 43726, 69292, 21656, 32427, 2402, 7747, 1720, 9151, 60491, 1371, 7077,
CC 33207, 1419, 18036, 16105, 38650, 14245, 58548, 1870, 25856, 32394, 3484,
CC 345, 9252, 9135, 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912,
CC 2868, 283, 2534, 9464, 17799, 26686, 43948, 32135, 12208, 2914, 51130,
CC 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474, 9792, 15400, 1452 or
CC 6585 genes in cardiovascular disease states. The methods are useful in
CC diagnosing, preventing and treating cardiovascular disorders, such as
CC atherosclerosis, cardiac hypertrophy, ischaemia, reperfusion injury,
CC restenosis, arterial inflammation, vascular wall remodeling, coronary
CC microembolism, tachycardia, bradycardia, pressure overload, aortic
CC bending, coronary artery ligation, vascular heart disease, valvular
CC disease, including but not limited to, valvular degeneration caused by
CC calcification, rheumatic heart disease, endocarditis, or complications of
CC artificial valves; atrial fibrillation, long-QT syndrome, congestive
CC heart failure, sinus node dysfunction, angina, heart failure,
CC hypertension, atrial fibrillation, atrial flutter, pericardial disease,
CC including but not limited to, pericardial effusion and pericarditis;
CC cardiomyopathies, e.g. dilated cardiomyopathy or idiopathic
CC cardiomyopathy, myocardial infarction, coronary artery disease, coronary
CC artery spasm, ischaemic disease, arrhythmia, sudden cardiac death and
CC cardiovascular developmental disorders. The methods may also be used for
CC identifying compounds that modulate cardiovascular disorders. Sequences
CC given in ADE31644-ADE31769 represent the genes and proteins that may be
CC regulated by a compound of the invention.

XX Sequence 352 AA;

Query Match 88.5%; Score 1727; DB 7; Length 352;
Best Local Similarity 99.4%; Pred. No. 8.9e-182;
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTAAALITLVRSQGNQVRRVLLSSRLQLDDRRVPTTCHSTSEPRCSRFPDGGSPAT 60
DB 1 MSTAAALITLVRSQGNQVRRVLLSSRLQLDDRRVPTTCHSTSEPRCSRFPDGGSPAT 60
QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLVNVCASQIGKRKENEDRFPDQAULTDEV 120
DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLVNVCASQIGKRKENEDRFPDQAULTDEV 120
QY 121 LYFVAVYDGHGGPAAADFCHTHMEKIMDLPLKPKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
DB 121 LYFVAVYDGHGGPAAADFCHTHMEKIMDLPLKPKNLETLTLTFLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVITDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSEFLVITDGI 300
QY 301 NFMVNSQEICDFVNQCHDPNEAAHVAETEQAIIQ 332

Db 301 NFMVNSQICDFVNOCHDPNEAAHVAETEQTQ 332
|||||

RESULT 21

ABBO7392
ID ABB07392 standard; protein; 373 AA.
XX
AC ABB07392;
XX
DT 09-APR-2002 (first entry)
XX
DE Human protein phosphatase IIC ABI2 polypeptide.
XX
KW Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
KW antiinflammatory; anabolic; cancer.
XX
OS Homo sapiens.
XX
FN WO200196571-A2.
XX
PD 20-DEC-2001.
XX
XX 13-JUN-2001; 2001WO-EP006666.
XX
XX 16-JUN-2000; 2000US-0212043P.
PR
XX 07-AUG-2000; 2000US-0223322P.
PR
XX 13-DEC-2000; 2000US-0254877P.
XX
PA (FARB) BAYER AG.
XX
XX Xiao Y;
PI
XX
XX WPI; 2002-139713/18.
DR
XX N-PSDB; ABA94569.
XX

PT Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
PT identifying modulating agents useful in treating diseases e.g. cancer,
PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
XX
XX Claim 26; Fig 2; 135pp; English.
XX
XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
XX and polynucleotides. The polypeptides can be expressed by standard
XX recombinant methodology. The polypeptides, polynucleotides and modulators
XX are useful for modulating activity of protein phosphatase IIC ABI2 in a
XX disease or treating a disease which include asthma, chronic obstructive
XX pulmonary disease (COPD), peripheral or central nervous system disease
XX including neurodegenerative disease, a disorder associated with an
XX increase in apoptosis, including AIDS and other infectious or genetic
XX immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
XX wasting disease, viral infection and osteoporosis; or disorder associated
XX with decrease in apoptosis, including cancer and inflammatory disorder.
XX Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
XX generating antibodies and for use in various assay systems, and the
XX protein phosphatase IIC ABI2 polypeptide can also be used as a bait
XX protein in a two-hybrid assay or three-hybrid assay. The present sequence
XX represents a human protein phosphatase IIC ABI2 polypeptide
XX
XX Sequence 373 AA;

Query Match 78.9%; Score 1538.5; DB 5; Length 373;
Best Local Similarity 85.6%; Pred. No. 7.3e-161;
Matches 303; Conservative 6; Mismatches 22; Indels 23; Gaps 3;
SQ
QY 1 MSTAALITLVRSQGVRRVLLSRLQDDRRVTPTCHSTSEPRCSRFPDGGSGPAT 60
Db 1 MSTAALITLVRSQGVRRVLLSRLQDDRRVTPTCHSTSEPRCSRFPDGGSGPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGRPIPKISLENVGCASQIGKRKXENEDRFDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGRPIPKISLENVGCASQIGKRKXENEDRFDFAQLTDEV 120

QY 121 LYFAVYDGHGGPAAADFCHTHMEKICMDLLPKENLETLLTLAFLEI----DKAFSSSHAR 176
Db 121 LYFAVYDGHGGPAAADFCHTHMEKICMFVM-FEHNSWVKFVFASVRVICGRELCVSSSR 179
QY 177 LSA-----DATLITSGTTATVALLRDGIELVVASVGSRAILCRKKG 218
Db 180 PGARGHYMRGFSKRDLLNFVPATLITSGTTATVALLRDGIELVVASVGSRAILCRKKG 239
QY 219 PMKLTIDHTPERKDEKERIKKCGFVAMNSLGQPHVNGRLAMTRS:GDLDLKTSGVIAEP 278
Db 240 PMKLTIDHTPERKDEKERIKKCGFVAMNSLGQPHVNGRLAMTRS:GDLDLKTSGVIAEP 299
QY 279 ETXRIKLHADDGFLVLTDTGINFVMSQICDFVNOCHDPNEAAHVAETEQTQ 332
Db 300 ETXRIKLHADDGFLVLTDTGINFVMSQICDFVNOCHDPNEAAHVAETEQTQ 353

RESULT 22

ABG06716
ID ABG06716 standard; protein; 1072 AA.
XX
AC ABG06716;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #6707.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
OS
XX WO200175067-A2.
FN
XX 11-OCT-2001.
PD
XX 30-MAR-2001; 2001WO-US008631.
PF
XX 31-MAR-2000; 2000US-00540217.
PR
XX 23-AUG-2000; 2000US-00649167.
PR
XX (HYSE-) HYSEQ INC.
FA
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR
XX N-PSDB; AAS70903.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 20; SEQ ID NO 37075; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 1072 AA;
SQ

Query Match	70.5%;	Score 1375.5;	DB 4;	Length 1072;
Best Local Similarity	46.5%;	Pred. No. 4.6e-142;		
Matches 302; Conservative	6;	Mismatches 20;	Indels 321;	Gaps 4;

QY

1 MSTAALITLVRSGGNQVRRRVLLSSRLQLDDRRVTPTCHSSTSPRCSRFPDGGSPAT 60
| | | | |
D6

1 MSTAALITLVRSGGNQVRRRVLLSSRLQLDDRRVTPTCHSSTSPRCSRFPDGGSPAT 60
| | | | |

Qy 61 WDNFGIWDNRIDEPILLPPSIKYCKGPIKXISLNVGCASQIGKKENEDRDFEQLTDEV 120
 |
 |
 |
Db 61 WDNFGIWDNRIDEPILLPPSIKYCKGPIKXISLNVGCASQIGKKENEDRDFEQLTDEV 120
 |
 |
 |

Qy 121 LYFVYDCHGGPAAADFCHTHMEKCINDLLPKEKNLETLTLAPLEI----DKAFSSSHR 176
 |||||
 Db 121 LYFVYDCHGGPAAADFCHTHMEKCIEMVM-FPHNSWKEFVFAVRVIGRELCIVSSSR 179
 |||||

Qy	177	LSA-----	-----	DATLLTSGTTATVALLRDLIELVAVSGDSRAILCRKCK	218
nb	180	DGAPCHVMBGFCSCVDNI	INIEVBATLITSGTTATVALLRDLIELVAVSGDSRAILCRKCK	219	

QY 219 PMKLTIDHTPERKDEKERIKKCGGFVANNLSGQPHVNSGLAMTRISIGDLDLKTSGVIAEP 278

nb 240 DMKLTITIDHTDEPDVDFEYETKKCCGCEVANNLSGQPHVNSGLAMTRISIGDLKTSGVIAEP 299

Qy	279 ETKRIK-----	284
200	ETKRIK-----	250

Qy 285 ----- 284

Qy 285
..... 284

Qy ----- 285 ----- 284 -----

Qy 285 284

285 ----LHRADDSFVLTTDGINFMVNSQETCDFVNQCHDPNEAAHAATVEQ 329

RESULT 23

ABG28412
ID ABG28412 standard; protein; 1195 AA.
XX
AC ABG28412;

18-FEB-2002 (first entry)
Novel human diagnostic protein #28403.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
KW
XX

OS	Homo sapiens.
XX	
PN	WC200175067-A2.
YY	

11-OCT-2001.
30-MAR-2001; 2001WO-US008631.
31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00643167.
(HYSE-) HYSEQ INC.
Drmanac RT, Liu C, Tang YT;
WPI; 2001-639362/73.
N-PSDB; AAS92599.
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity.
Claim 20; SEQ ID NO 58771; 103pp; English.
The invention relates to isolated polynucleotide (I) and polypeptide (II)
sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
supplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving aberrant protein expression or biological activity. The
polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic
amino acid sequences of the invention. Note: The sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from Wipo at
ftp.wipo.int/pub/published_pct_sequences
Sequence 1195 AA;
SQ

Query Match	70.5%;	Score 1375.5;	DB 4;	Length 1195;
Best Local Similarity	46.5%;	Pred. No. 5.5e-142;		
Matches	302;	Conservative	6;	Mismatches 20; Indels 321; Gaps 4;
Qy	1	MSTAALITLVRSGNOVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDPDGGSGSPAT	60	
Db	1	MSTAALITLVRSGNOVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDPDGGSGSPAT	60	
Qy	61	WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASOIGRKKENEDRDFQAQLTDEV	120	
Db	61	WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASOIGRKKENEDRDFQAQLTDEV	120	
Qy	121	LYFAVYDGHGGPAAAFCHTHMEKCIIMDLPPKKNUETLTLTFLAFLI-----DKAFSSHAR	176	
Db	121	LYFAVYDGHGGPAAAFCHTHMEKCIIMFVM--FEHNSWVKVFASRVICGRELCVSSSR	179	
Qy	177	LSA-----DATTLTSGTTATVALLRDGIELVWASVGSRAILLCRKKG	218	
Db	180	PGARGHYMRGFSGRDLLNFPATLITSGTTATVALLRDGIELVWASVGSRAILLCRKKG	239	
Qy	219	PMKLTIDHTPERKDEKERIKKCGGFVAVNSLGGPHVNGRLANTRSIGDLDLKTSGVIAEP	278	
Db	240	PMKLTIDHTPERKDEKERIKKCGGFVAVNSLGGPHVNGRLANTRSIGDLDLKTSGVIAEP	299	
Qy	279	ETKRK-----	284	
Db	300	ETKRKLWNPSGPEVLLFFLTCTQASAITCTQCSITCTQSSITCTQASASPANQPASP	359	

Qy	285	-----	284
Db	360	APKQASAPAFSPQSPAPNPQASPTNPQFASAPNPQASLAPNPQASAPNPQ	419
Qy	285	-----	284
Db	420	PASPAPNPQSPAPNPQHLLHPISITCTQSPASPASSQSPASPAPNPQSPAPNPQHLLHPIS	479
Qy	285	-----	284
Db	480	TCTQSAAPAPSPQSPAPNPQHLLHTASITCTQSANITCTQSANITCTQSSITCTQSSI	539
Qy	285	-----	284
Db	540	TCTQSANITCTQSANITCTQSPASNPQLTNPQNPQSPAPNPQSPAPNPQHLLHPISQH	599
Qy	285	-----	284
Db	600	HLHPLHADDSEFLVLTGDFNFWNSQICDFVNOCHDPNEAAHATVEQ 648	
<p>RESULT 24</p> <p>AA41604</p> <p>ID AA41604 standard; protein; 238 AA.</p> <p>XX AA41604;</p> <p>XX 22-OCT-2001 (first entry)</p> <p>XX Human polypeptide SEQ ID NO 6535.</p> <p>XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;</p> <p>KW peripheral nervous system; neuropathy; central nervous system; CNS;</p> <p>KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;</p> <p>KW amyotrophic lateral sclerosis; Shy-Drager syndrome; chemotactic;</p> <p>KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;</p> <p>XX leukaemia.</p> <p>XX Homo sapiens.</p> <p>XX WO200153312-A1.</p> <p>XX 26-JUL-2001.</p> <p>XX 26-DEC-2000; 2000WO-US034263.</p> <p>XX 23-DEC-1999; 99US-00471275.</p> <p>XX 21-JAN-2000; 2000US-0048725.</p> <p>XX 25-APR-2000; 2000US-0052317.</p> <p>XX 20-JUN-2000; 2000US-00598042.</p> <p>XX 19-JUL-2000; 2000US-00620312.</p> <p>XX 03-AUG-2000; 2000US-00653450.</p> <p>XX 14-SEP-2000; 2000US-00662191.</p> <p>XX 19-OCT-2000; 2000US-00693036.</p> <p>XX 29-NOV-2000; 2000US-00727344.</p> <p>XX (HYSE-) HYSEQ INC.</p> <p>XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;</p> <p>PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;</p> <p>PI Zhou P, Goodrich R, Drmanac RT;</p> <p>XX WPI; 2001-442253/47.</p> <p>DR DR N-PSDB; AA160760.</p> <p>XX Novel nucleic acids and polypeptides, useful for treating disorders such</p> <p>PT as central nervous system injuries.</p> <p>XX Example 2; SEQ ID NO 6535; 10078pp; English.</p> <p>XX The invention relates to human nucleic acids (AA157798-AA161369) and the</p> <p>CC encoded polypeptides (AA138642-AA142213) with nootropic,</p> <p>CC immunosuppressant and cytostatic activity. The polynucleotides are useful</p>			

CC	in gene therapy. A composition containing a polypeptide or polynucleotide
CC	of the invention may be used to treat diseases of the peripheral nervous
CC	system, such as peripheral nervous injuries, peripheral neuropathy and
CC	localised neuropathies and central nervous system diseases, such as
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC	utilisation of the activities such as: Immune system suppression,
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC	assays for receptor activity, arthritis and inflammation, leukaemias and
CC	C.N.S disorders. Note: The sequence data for this patent did not form
CC	part of the printed specification
XX	
SQ	Sequence 238 AA;
	Query Match 58.9%; Score 1150; DB 4; Length 238;
	Best Local Similarity 99.6%; Pred. No. 3.7e-118;
	Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0
QY	148 DLLPEKKNLTLTLLAFLEIDKAPSSHARISADATLLTGTATTALLRDGIELVVASVG 207
DB	14 DLLPEKKNLTLTLLAFLEIDKAPSSHARISADATLLTGTATTALLRDGIELVVASVG 73
QY	208 DSRAILCRKGPKMLTIDHTPERKDEKERIKKCGGFVANNSLGQPHVNGRLAMTRSIGDL 267
DB	74 DSRAILCRKGPKMLTIDHTPERKDEKERIKKCGGFVANNSLGQPHVNGRLAMTRSIGDL 133
QY	268 DLKTSGVTAEPETKRIKLHADDSFLVLTDTGINFWMNISOEICDFYNQCHDPNEAAHAVT 327
DB	134 DLKTSGVTAEPETKRIKLHADDSFLVLTDTGINFWMNISOEICDFYNQCHDPNEAAHAVT 193
QY	328 EQAIOGYGEDNSTAVVPFFGAWGKYKNSEINFSPFSASSGRWA 372
DB	194 EQAIOGYGEDNSTAVVPFFGAWGKYKNSEINFSPFSASSGRWA 238
RESULT 25	
AAB47431	
ID	AAB47431 standard; protein; 233 AA.
XX	
AC	AAB47431;
XX	
DT	31-OCT-2001 (first entry)
XX	
DE	Human protein phosphatase 2C26.
XX	
KW	Human; protein phosphatase 2C26; diagnosis; malignant tumor; hemopathy;
KW	human immunodeficiency virus; HIV; inflammation.
XX	
OS	Homo sapiens.
XX	
PN	WO200155425-AI.
XX	
PD	02-AUG-2001.
XX	
Pf	15-JAN-2001; 2001WO-CN000054.
XX	
PR	26-JAN-2000; 2000CN-00111524.
XX	
PA	(BIOD-) BIODOOR GENE TECHNOLOGY LTD SHANGHAI.
PI	Mao Y, Xie Y;
XX	
DR	WPI; 2001-483265/52.
XX	N-PSDB; AAH49207.
PT	Human protein phosphatase 2C26 and encoded polynucleotide, used in
PT	diagnosis and treatment of malignant tumors, hemopathy, human
PT	immunodeficiency virus infection, immunological diseases and
PT	inflammation.
XX	
XX	Claim 1; Page 27; 33pp; Chinese.
PS	
XX	

CC This sequence shows human protein phosphatase 2C26. The polypeptide and
CC encoded polynucleotide may be used in diagnosis and treatment of
CC malignant tumors, hemopathy, human immunodeficiency virus (HIV)
CC infection, immunological diseases and inflammation
XX
SQ Sequence 233 AA;

Query Match 48.8%; Score 951.5; DB 4; Length 233;
Best Local Similarity 86.6%; Pred. No. 3.4e-96;
Matches 187; Conservative 5; Mismatches 17; Indels 7; Gaps 1;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRDPDQSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRDPDQSGSPAT 60

Qy 61 WDNFGIWNRIDEPILPPSIKYKPKIPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120
Db 61 WDNFGIWNRIDEPILPPSIKYKPKIPKISLENVGCASQIGRKENEDRFDPAQLTDEV 120

Qy 121 LYFAVYDGHGGAADFCHTHMEKIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180
Db 121 LYFAVYDGHGGAADFCHTHMEKIMDLLPKENKLETLTLTFLAFLDKAFSSHARLSAD 180

Qy 181 ATLLTSGT-----TATVALLRDIQELVVASVGDS 209
Db 181 ENCAWSAALDPEVDITCGASVEREICLLSQVKES 216

RESULT 26
AAM39818
ID AAM39818 standard; protein; 153 AA.
AC
AC AAM39818;
XX
XX
XX 22-OCT-2001 (first entry)
XX
XX Human polypeptide SEQ ID NO 2963.
XX
XX Homo sapiens.
XX OS
XX WOZ00153312-Al.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
XX
XX N-PSDB; AAI58974.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.
XX
XX Example 4; SEQ ID NO 2963; 10078bp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 153 AA;

Query Match 41.7%; Score 8.4; DB 4; Length 153;
Best Local Similarity 100.0%; Pred. No. 2.9e-81;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 220 MKLTIDHTPERDEKERIKKCGGFVAMNSLGGPHVNGSLAMTRSIGDLDLKTSGVIAEPE 279
Db 1 MKLTIDHTPERDEKERIKKCGGFVAMNSLGGPHVNGSLAMTRSIGDLDLKTSGVIAEPE 60

Qy 280 TKRIKLHADDSEFLVLTITDGINFMVNSQIEICDFVNQCHDPNEAAHVAHQIYQCTEDNS 339
Db 61 TKRIKLHADDSEFLVLTITDGINFMVNSQIEICDFVNQCHDPNEAAHVAHQIYQCTEDNS 120

Qy 340 TAVVYVPGNGWYKNSSEINFSPSRFASGGWA 372
Db 121 TAVVYVPGNGWYKNSSEINFSPSRFASGGWA 153

RESULT 27
ADA55670
ID ADA55670 standard; protein; 150 AA.
XX
XX ADA55670;
XX
XX 20-NOV-2003 (first entry)
XX
XX Human protein, SEQ ID 3238.
XX
XX Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
XX Gene Therapy; human; secretory protein; membrane proteins; cancer;
XX inflammatory disease; osteoporosis; neurological disease.
XX
XX Homo sapiens.
XX
XX EP1293569-A2.
XX
XX 19-MAR-2003.
XX
XX 21-MAR-2002; 2002EP-00006586.
XX
XX 14-SEP-2001; 2001JP-00328381.
XX 24-JAN-2002; 2002US-0350435P.
XX
XX (HELI-) HELIX RES INST.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Iehli S;
XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
XX WPI; 2003-395539/38.
XX
XX N-PSDB; ADA54031.
XX
XX DR

XX New polynucleotides encoding full-length polypeptides, e.g. secretory
 PT and/or membrane proteins, useful for developing medicines for diseases in
 PT which the gene is involved, or as target molecules for gene therapy.

PS Claim 14; SEQ ID NO 3238; 205pp; English.

XX The present invention relates to novel human secretory or membrane
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
 CC ADA54071). The coding sequences are useful in the gene therapy of
 CC diseases caused by abnormalities of the proteins, e.g. cancer,
 CC inflammatory diseases, osteoporosis or neurological disease.

XX Sequence 150 AA;

Query Match 40.5%; Score 790; DB 6; Length 150;
 Best Local Similarity 100.0%; Pred. No. 1.3e-78;
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNVRRVRLLSRLQDDRRVTPTCHSSTSEPRCSRFDPDGGSPAT 60

DB 1 MSTAALITLVRSQGNVRRVRLLSRLQDDRRVTPTCHSSTSEPRCSRFDPDGGSPAT 60

QY 61 WDNFGIWNDRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEEDRFDFALITDEV 120

DB 61 WDNFGIWNDRIDEPILLPSIKYKPIPKISLENVGCASQIGKRKENEEDRFDFALITDEV 120

QY 121 LYFVAVYDGHGGPAAADFCHTHMEKICIM 147

DB 121 LYFVAVYDGHGGPAAADFCHTHMEKICIM 147

RESULT 28

ABB07393
 ID ABB07393 standard; protein; 156 AA.

XX ABB07393;

XX 09-APR-2002 (first entry)

DE Human protein phosphatase IIC ABI2 polypeptide.

XX Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
 KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
 KW antiinflammatory; anabolic; cancer.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "encoded by CAN"

FT Misc-difference 9 /note= "encoded by TGA"

FT Misc-difference 14 /note= "encoded by A"

XX WO200196571-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-EP006666.

XX 16-JUN-2000; 2000US-0212043P.

XX 07-AUG-2000; 2000US-0223322P.

XX 13-DEC-2000; 2000US-0254877P.

XX (FARB) BAYER AG.

XX Xiao Y;

XX WPI; 2002-139713/18.

XX N-PSDB; ABA94570.

PT Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX Claim 37; Fig 4; 135pp; English.

XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide

XX Sequence 156 AA;

Query Match 34.3%; Score 669.5; DB 5; Length 156;

Best Local Similarity 95.7%; Pred. No. 3e-65;

Matches 132; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 182 TLLTSGTTATVALLRDGIELVWASVGDSEAILCRKPKMLTIDHTPERKDEKRIKKG 241

DB 19 TLLTSGTTATVALLRDGIELVWASVGDSEAILCRKPKMLTIDHTPERKDEKRIKKG 78

QY 242 GFVWNSL-GQPHVNGRLWATRSIGDLTKTSVIAEPETKIKLHHADDSFLVLTDDGI 300

DB 79 GFVWNSLWGLTVNGRLWATRSIGDLTKTSVIAEPETKIKLHHADDSFLVLTDDGI 138

QY 301 NFMVNSQEICDFVNOCHD 318

DB 139 NFMVNSQEICDFVNOCHD 156

RESULT 29

ABB07397
 ID ABB07397 standard; protein; 83 AA.

XX ABB07397;

XX 09-APR-2002 (first entry)

DT Human protein phosphatase IIC ABI2 polypeptide.

DE Protein phosphatase IIC ABI2; antiasthmatic; antiapoptotic; anti-HIV;
 KW neuroprotective; vasotropic; virucide; osteopathic; cytostatic; human;
 KW antiinflammatory; anabolic; cancer.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 72 /note= "encoded by ANC"

XX WO200196571-A2.

XX 20-DEC-2001.

XX 13-JUN-2001; 2001WO-EP006666.

XX 16-JUN-2000; 2000US-0212043P.

XX 07-AUG-2000; 2000US-0223322P.

XX 13-DEC-2000; 2000US-0254877P.

XX (FARB) BAYER AG.

XX Xiao Y;
PI WPI; 2002-139713/18.
DR N-PSDB; ABA94574.
XX
PT Protein phosphatase IIC ABI2 polypeptide and polynucleotides useful for
PT identifying modulating agents useful in treating diseases e.g. cancer,
PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
XX
PS Claim 37; Fig 12; 135pp; English.
XX
CC The invention relates to human protein phosphatase IIC ABI2 polypeptides
CC and polynucleotides. The polypeptides can be expressed by standard
CC recombinant methodology. The polypeptides, polynucleotides and modulators
CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
CC disease or treating a disease which include asthma, chronic obstructive
CC pulmonary disease (COPD), peripheral or central nervous system disease
CC including neurodegenerative disease, a disorder associated with an
CC increase in apoptosis, including AIDS and other infectious or genetic
CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
CC wasting disease, viral infection and osteoporosis; or disorder associated
CC with decrease in apoptosis, including cancer and inflammatory disorder.
CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
CC generating antibodies and for use in various assay systems, and the
CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
CC represents a human protein phosphatase IIC ABI2 polypeptide
XX
SQ Sequence 83 AA;

Query Match 22.4%; Score 437; DB 5; Length 83;
Best Local Similarity 98.8%; Pred. No. 6e-40;
Matches 82; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 283 IKLHADSFLVLTGDNFVYNSQEICDFVNCQCHDPNEAAHVAETQAIQYGTEDNSTAV 342
Db 1 IKLHADSFLVLTGDNFVYNSQEICDFVNCQCHDPNEAAHVAETQAIQYGTEDNSTAV 60

QY 343 VVFGAGKXKXSEINFSSRSF 365
Db 61 VVFGAGKXKXSEINFSSRSF 83

RESULT 30
AAG06997
XX ID AAG06997 standard; protein; 354 AA.
XX AC AAG06997;
XX
XX 17-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 3980.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EP1033405-A2.
XX
XX 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
XX 23-MAR-1999; 99US-0125788P.
XX 25-MAR-1999; 99US-0126264P.
XX 29-MAR-1999; 99US-0126785P.
XX 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
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PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
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PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.

PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
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PR 30-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
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PR 06-MAY-1999; 99US-0132486P.
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PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136382P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
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PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
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PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
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PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154032P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.

QY 335 TEDNSTAVVVPFGWGKYKNSIN 358
 ID ABB07400 standard; protein; 423 AA.
 XX ABB07400;
 AC ABB07400;
 XX
 DT 09-APR-2002 (first entry)
 XX
 DE Amino acid sequence of protein seq Id No. 16 (Swiss Prot No. 004719).
 XX
 KW Protein phosphatase IIC AB12; antiasthmatic; antiapoptotic; anti-HIV;
 KW neuroprotective; vasotrophic; virucide; osteopathic; cytostatic; human;
 KW antiinflammatory; anabolic; cancer.
 XX
 OS Homo sapiens.
 XX
 XX WO200196571-A2.
 FN
 XX
 PD 20-DEC-2001.
 XX
 PF 13-JUN-2001; 2001WO-EP006666.
 XX
 PR 16-JUN-2000; 2000US-0212043P.
 PR 07-AUG-2000; 2000US-0223322P.
 PR 13-DEC-2000; 2000US-0254877P.
 XX
 PA (FARB) BAYER AG.
 XX
 XX Xiao Y;
 PI
 XX
 DR WPI; 2002-139713/18.
 XX
 PT Protein phosphatase IIC AB12 polypeptide and polynucleotides useful for
 PT identifying modulating agents useful in treating diseases e.g. cancer,
 PT inflammatory disorder, osteoporosis, asthma, AIDS and viral infections.
 XX
 PS Claim 37; Fig 16; 135pp; English.
 XX
 CC The invention relates to human protein phosphatase IIC AB12 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC AB12 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis, or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC AB12 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC AB12 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents the amino acid sequence of protein identified with Swiss Prot
 CC Accn No. 004719
 XX
 SQ Sequence 423 AA;
 Query Match 18.2%; Score 354.5; DB 5; Length 423;
 Best Local Similarity 30.6%; Pred. No. 1.2e-29;
 Matches 99; Conservative 51; Mismatches 99; Indels 75; Gaps 12;
 QY 96 GCASQIGKKNRFRD-----FAQLTDEVL-----YFAYVDHGGA 135
 DB 114 GVTSCGRPEMEDSVSTIPFLQVSSSLDGRVTNGFNPHLSAHFFGVYDGHGSGVA 173
 QY 136 DFCHTHMEKCMIDLPLKPK-----NLETLTLAFLEIDKAFSSSHARLSADATLL 184

Db 174 NYCRRMHLALTEEIVKEKPEFCGDTWQEKWKALFNSFMRVDSIETVAHAPE----- 228
 QY 185 TSCTTATVALLRDGIELVVASVDSRAILCRKGKMKLTIDHTPERKDKERIKKCGG-P 243
 Db 229 TVGTSVAVVFP-THIFVANGDSRAVLCKRTPLALSVDHKPDDEAAREAAAGKV 287
 QY 244 VAVNSLQGPVNGRLAMTRISIGDLDKTSGVIAEPE---TKRIKHHADDSFLVLTDDGI 300
 Db 288 IRWNG--ARVFGVLAMSRISIGDYLKPS-VIPDPEVTSVRRVK-----EDDCILIASDGL 339
 QY 301 NFMVNSQEICDFVNQ-----CHDPN-----EAAHAYTEQAIQYG 334
 Db 340 WDVMTNEEVCDIARKRILLWHKKNWAGRALLPAEKRGEGKDPAAAMSAAYLSKMAQLQK 399
 QY 335 TEDNSTAVVVPFGWGKYKNSIN 358
 Db 400 SKDNISVVVVDLKGIRKFKSKSLN 423
 RESULT 34
 AAE04841
 ID AAE04841 standard; protein; 360 AA.
 XX
 AC AAE04841;
 XX
 DT 10-SEP-2001 (first entry)
 XX
 DE Human SGP039 phosphatase polypeptide.
 XX
 KW Human; SGP039 phosphatase polypeptide; phosphatase-related disease;
 KW immune-related disorder; ocular disease; organ transplant rejection;
 KW infection; diabetes; pain; sexual dysfunction; Alzheimer's disease;
 KW metabolic disorder; haematopoietic cancer; mood disorder; cardiac;
 KW Parkinson's disease; multiple sclerosis; amyotrophic lateral sclerosis;
 KW cardiovascular disease; brain; neuronal-associated disease; dyskinesia;
 KW attention disorder; cognition disorder; psychotic disorder; cytostatic;
 KW neurological disorder; virucide; nootropic; cerebrotective; therapy;
 KW neuroprotective; antibacterial; vulnary; tranquilliser; aniastrmatic;
 KW hypotensive; immunosuppressive; antipsoriatic; analgesic; hypertensive;
 KW antifungal; migraine; serine phosphatase; Srp; PP2C.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..301
 FT /label= Catalytic_domain
 FT Domain 91..344
 FT /label= Phosphatase_domain
 XX WO200146394-A2.
 PN
 PD 28-JUN-2001.
 XX
 PF 21-DEC-2000; 2000WO-US034736.
 XX
 PR 21-DEC-1999; 99US-0173255P.
 PR 28-DEC-1999; 99US-0175766P.
 PR 25-JAN-2000; 2000US-0178078P.
 PR 31-JAN-2000; 2000US-0179301P.
 XX
 XX (SUGB-) SUGEN INC.
 PA
 XX Plowman GD, Martinez R, Whyte D, Manning G, Sudarsanam S;
 PI Hill RJ, Flanagan P;
 XX WPI; 2001-418058/44.
 DR N-PSDB; AAD09493.
 XX Novel phosphatase polypeptide useful for treating cancers, immune-related
 PT diseases and disorders, cardiovascular disease, brain or neuronal-
 PT associated diseases and metabolic disorders.
 XX
 PS Claim 7; Fig 2; 186pp; English.

FT	Region	89. .349
FT	/note= "Protein phosphatase 2C"	
FT	Region	91. .344
FT	/note= "Protein phosphatase 2C Pp2"	
FT	Region	97. .360
FT	/note= "Protein phosphatase 2C"	
FT	Region	97. .276
FT	/note= "Protein phosphatase 2C magnesium hydrolase manganese multigene family PP2C isoform"	
FT	Region	99. .109
FT	/note= "Protein phosphatase 2C p"	
FT	Region	123. .132
FT	/note= "Protein phosphatase 2C p"	
FT	Region	123. .131
FT	/note= "Protein phosphatase 2C Pp2c"	
FT	Region	210. .249
FT	/note= "Protein phosphatase 2C p"	
FT	Region	256. .269
FT	/note= "Protein phosphatase 2C p"	
FT	Region	294. .306
FT	/note= "Protein phosphatase 2C p"	
FT	Region	340. .349
FT	/note= "Protein phosphatase 2C p"	
XX	W0200210363-A2.	
PX	PN	XX
XX	07-FEB-2002.	
XX	26-JUL-2001; 2001WO-US023716.	
PP		
XX	28-JUL-2000; 2000US-0221679P.	
PR	03-AUG-2000; 2000US-0223272P.	
PR	10-AUG-2000; 2000US-0224309P.	
PR	18-AUG-2000; 2000US-0226728P.	
PR	30-AUG-2000; 2000US-0229254P.	
PR	08-SEP-2000; 2000US-0231366P.	
XX	(INCY-) INCYTE GENOMICS INC.	
PA	Tang YT, Elliott VS, Ramkumar J, Yao MG, Burford N, Wang YE; Stewart EA, Gandhi AR, Patterson C, Lee EA, Hafalia AJA, Lu DAM; Triboley CM, Griffin JA, Baughn KR, Yue H, Warren BA, Nguyen DB; Malik NK, Kearney L;	
XX	WPI; 2002-188735/24.	
DR	N-PSDB; ABK14469.	
XX	New protein phosphatases, useful for diagnosing, treating or preventing immune system disorders (e.g. Crohn's disease), neurological disorders (e.g. Parkinson's disease), or cell proliferative disorders (e.g. cancers).	
PT	Claim 1; Page 102; 117pp; English.	
FT	The present invention relates to a new polypeptide, a naturally occurring amino acid sequence at least 95 % identical to it, a biologically active fragment of it or an immunogenic fragment of it. The polypeptides, polynucleotides, agonists and antagonists are useful for diagnosing, treating or preventing disorders associated with aberrant expression of protein phosphatases (PP), particularly immune system disorders e.g. acquired immunodeficiency syndrome (AIDS), thymic hypoplasia, anaemia, asthma or Crohn's disease, neurological disorders e.g. epilepsy, Huntington's disease, dementia or Parkinson's disease, developmental disorders e.g. Down's syndrome, or cell proliferative disorders e.g. cancers including adenocarcinoma, leukaemia, lymphoma, melanoma, myeloma or sarcoma. The present amino acid sequence represents human protein phosphatase 2 (PP2) which is one of several human protein phosphatases (AAU5783-AAU5792) of the invention	
XX	Sequence 360 AA;	
XX	Query Match 18.0%; Score 350.5; DB 5; Length 360;	
XX	Best Local Similarity 34.3%; Fred No. 2.5e-29;	

XX Claim 37; Fig 14; 135pp; English.
 XX The invention relates to human protein phosphatase IIC ABI2 polypeptides
 CC and polynucleotides. The polypeptides can be expressed by standard
 CC recombinant methodology. The polypeptides, polynucleotides and modulators
 CC are useful for modulating activity of protein phosphatase IIC ABI2 in a
 CC disease or treating a disease which include asthma, chronic obstructive
 CC pulmonary disease (COPD), peripheral or central nervous system disease
 CC including neurodegenerative disease, a disorder associated with an
 CC increase in apoptosis, including AIDS and other infectious or genetic
 CC immunodeficiency, myelodysplasia, ischemic injury, toxin-induced disease,
 CC wasting disease, viral infection and osteoporosis; or disorder associated
 CC with decrease in apoptosis, including cancer and inflammatory disorder.
 CC Fusion proteins comprising protein phosphatase IIC ABI2 are useful for
 CC generating antibodies and for use in various assay systems, and the
 CC protein phosphatase IIC ABI2 polypeptide can also be used as a bait
 CC protein in a two-hybrid assay or three-hybrid assay. The present sequence
 CC represents a human protein phosphatase IIC ABI2 polypeptide
 XX
 SQ Sequence 76 AA;
 Query Match 17.8%; Score 348; DB 5; Length 76;
 Best Local Similarity 98.5%; Pred. No. 3.7e-30;
 Matches 66; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 234 KERIKKGGFVAVNSLQGPVHNGRLAMTRSIGDLKTSQVIAEPETKRIKLHHADDSFL 293
 DB 1 KERIKKGGFVAVNSLQGPVHNGRLAMTRSIGDLKTSQVIAEPETKRIKLHHADDSFL 60
 QY 294 VLTTDGI 300
 DB 61 VLTTDGL 67
 RESULT 38
 AAE01349
 ID AAE01349 standard; protein; 423 AA.
 AC AAE01349;
 XX 31-JUL-2001 (first entry)
 DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 2, abi2 mutant.
 XX
 KW Abscisic acid; ABA; ABA-insensitive, abi2; signal transduction;
 KW kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;
 KW tomato; pine; soybean; peanut; olive; mutant; mutein.
 XX
 OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 168
 FT /note= "Wild type Gly substituted with Asp"
 XX
 PN W0200136596-A2.
 XX
 PD 25-MAY-2001.
 XX
 PF 17-NOV-2000; 2000WO-US031739.
 XX
 PR 17-NOV-1999; 99US-0166080P.
 XX
 PA (PION-) PIONEER HI-BRED INT INC.
 XX
 PI Helentjaris T;
 XX
 DR WPI; 2001-329218/34.
 DR N-PSDB; AAD05668.
 XX
 PT DNA constructs containing an abscisic acid-associated sequence are used
 PT to modulate a response in a plant to abscisic acid so that the plants are
 PT protected against any harmful or detrimental effects of stress and

environmental conditions.
 XX Claim 5; Page; 60pp; English.
 XX The invention relates to a method for modulating a response in a target
 CC plant to abscisic acid (ABA) by introducing a DNA construct comprising an
 CC ABA-associated sequence operably linked to an early kernel/embryo
 CC promoter into the plant. The method also involves modulating ABA
 CC perception and signal transduction in developing seeds. The method is
 CC used to produce plants, particularly cereal plants such as maize, which
 CC have a modified response to ABA so that an increase in yield can be
 CC produced. The plants are protected against any harmful/detrimental
 CC effects of stress and adverse environmental conditions. The ABA function
 CC is disrupted in a tissue and developmental preferred manner so that
 CC female reproductive tissue is insulated from the stress or adverse
 CC environmental conditions. Other plants which can be transformed include
 CC rice, cotton, citrus trees, tomatoes, pines, soybean, peanut and olive.
 CC The present sequence is Arabidopsis thaliana ABA-insensitive 2 (abi2)
 CC mutant. Note: The present sequence is not shown in the specification but
 CC is derived from ABI2 protein referred as SED ID NO: 6 (AAE01345) and
 CC shown in sequence listing of the specification
 XX
 SQ Sequence 423 AA;
 Query Match 17.8%; Score 347.5; DB 4; Length 423;
 Best Local Similarity 30.2%; Pred. No. 6.9e-29;
 Matches 98; Conservative 51; Mismatches 100; Indels 75; Gaps 12;
 QY 96 GCASQIGKXKXENEDRPD---FAQLTDEVL-----VFAYVDGHGGPAAA 135
 DB 114 GVTISICGRPEMEDSVSTIPRFLOVSSSSLLDGRVNGFNPHLSAHFFGYDGHDSQVA 173
 QY 136 DFCHTHMEKICIMDLLPKK-----NLETLLTFLALETIDKAFSSHARLSADATLL 184
 DB 174 NYCSERMHLATBEIVKEPEKFCGDTGWTQEKWKALKFNSEFMVDSLETVAHAPE----- 228
 QY 185 TSGTTATVALLRDGIELAVASVGSRAILCRKPKMKLTIDHTPERKDEKRIKCGG-F 243
 DB 229 TVGSTVAVVFP-THIFVANGDSRAVLCRGKGTPLALSVDHPRDDEARLEAGGKV 287
 QY 244 VAMNSLQGPVHNGRLAMTRSIGDLKTSQVIAEPE---TKRIKLHHADDSFLVLTDDGI 300
 DB 288 IRWNG---ARVFGVLAWSRSIGDRYLKPS-VI PDPEVTSVRRVK---EDDCILASDGL 339
 QY 301 NFMVNSOEICDFVNO-----CHDPN-----EAAHAVTEQAIQVG 334
 DB 340 WDVMTNEVCDLARKRILLWHEKKNAMAGEALLPAEKKGEGKDPAAWSAAEYLSKMALQKG 399
 QY 335 TEDNSTAVVVPFGAWGKYKNSIN 358
 DB 400 SKDNISVVVDLKGIRKFKSKSLN 423
 RESULT 39
 AAG06998
 ID AAG06998 standard; protein; 309 AA.
 AC AAG06998;
 XX 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 3981.
 XX
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX
 OS Arabidopsis thaliana.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX

PF 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 05-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 23-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
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PR 01-JUN-1999; 99US-0137223P.
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PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.	PR	29-OCT-1999;	99US-0162143P.
PR	05-AUG-1999;	99US-0147192P.	PR	29-OCT-1999;	99US-0162144P.
PR	05-AUG-1999;	99US-0147260P.	PR	29-OCT-1999;	99US-0162145P.
PR	06-AUG-1999;	99US-0147303P.	PR	29-OCT-1999;	99US-0162146P.
PR	06-AUG-1999;	99US-0147416P.	PR	29-OCT-1999;	99US-0162147P.
PR	09-AUG-1999;	99US-0147493P.	PR	29-OCT-1999;	99US-0162148P.
PR	09-AUG-1999;	99US-0147935P.	PR	29-OCT-1999;	99US-0162149P.
PR	10-AUG-1999;	99US-0148171P.	PR	29-OCT-1999;	99US-0162150P.
PR	11-AUG-1999;	99US-0148319P.	PR	29-OCT-1999;	99US-0162151P.
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PR	13-AUG-1999;	99US-0148684P.	PR	29-OCT-1999;	99US-0162154P.
PR	16-AUG-1999;	99US-0149366P.	PR	29-OCT-1999;	99US-0162155P.
PR	17-AUG-1999;	99US-0149175P.	PR	29-OCT-1999;	99US-0162156P.
PR	18-AUG-1999;	99US-0149426P.	PR	29-OCT-1999;	99US-0162157P.
PR	20-AUG-1999;	99US-0149722P.	PR	29-OCT-1999;	99US-0162158P.
PR	20-AUG-1999;	99US-0149723P.	PR	29-OCT-1999;	99US-0162159P.
PR	23-AUG-1999;	99US-0149929P.	PR	29-OCT-1999;	99US-0162160P.
PR	23-AUG-1999;	99US-0149902P.	PR	29-OCT-1999;	99US-0162161P.
PR	23-AUG-1999;	99US-0149903P.	PR	29-OCT-1999;	99US-0162162P.
PR	23-AUG-1999;	99US-0149904P.	PR	29-OCT-1999;	99US-0162163P.
PR	25-AUG-1999;	99US-0150566P.	PR	29-OCT-1999;	99US-0162164P.
PR	26-AUG-1999;	99US-0150884P.	PR	29-OCT-1999;	99US-0162165P.
PR	27-AUG-1999;	99US-0151065P.	PR	29-OCT-1999;	99US-0162166P.
PR	27-AUG-1999;	99US-0151066P.	PR	29-OCT-1999;	99US-0162167P.
PR	27-AUG-1999;	99US-0151080P.	PR	29-OCT-1999;	99US-0162168P.
PR	30-AUG-1999;	99US-0151303P.	PR	29-OCT-1999;	99US-0162169P.
PR	31-AUG-1999;	99US-0151438P.	PR	29-OCT-1999;	99US-0162170P.
PR	01-SEP-1999;	99US-0151930P.	PR	29-OCT-1999;	99US-0162171P.

Query Match 17.6%; Score 343.5; DB 3; Length 294;
Best Local Similarity 35.4%; Pred. No. 1.1e-28;
Matches 96; Conservative 43; Mismatches 87; Indels 45; Gaps 9;
QY 98 ASQIGKRENERDFPAQLTDEVLPYAVYDGHGPPAAADFCHTHMEKICIMDLLPKE---- 153
DB 12 SSQVG-----SLFELPKPSAFVAVFDGHGPEAAAYVR---ENAIRFFEDRQFPQ 59
QY 154 -----KNLETLTLTFLAFLIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVA 204
DB 60 TSEVSSVYVEVETSRLNAPLQADALAEDCSISD-----SCGTTALTALI-CGRLLAWA 113
QY 205 SVGDSRAILCRKGPMLKLTIDHTPERKDEKIRIKOGGFVAVNSLQOPHVNGRLAMTRSI 264
DB 114 NAGDCRAVLCKRGRAIDMSDEHKPINLERRAVEESGGFIT---NDGYLNEVLAVTRAL 169
QY 265 GDLDLK-----TSGVIAETPKRIKULHADDGFLVLTTCGINFVWNSQEICDFV-----NQ 315
DB 170 GMDLKLPHGQSPLISEPIKQITLTDDEFLVTGCDGIDWDLTSSQBAVSIVRRLGR 228
QY 316 CHDPNEAAHVAETQALQYGTEDNNTAVVVPF 346
DB 229 HNDPTRCARELWNEALGRNSFDNLTAIVVYCF 259

RESULT 41
AAG-8039

PR	23-AUG-1999;	99US-0149830P.	
PR	25-AUG-1999;	99US-0150566P.	
PR	26-AUG-1999;	99US-0150884P.	
PR	27-AUG-1999;	99US-0151065P.	
PR	27-AUG-1999;	99US-0151066P.	
PR	27-AUG-1999;	99US-0151080P.	
PR	30-AUG-1999;	99US-0151303P.	
PR	31-AUG-1999;	99US-0151438P.	
PR	01-SEP-1999;	99US-0151930P.	
PR	07-SEP-1999;	99US-0152363P.	
PR	10-SEP-1999;	99US-0153070P.	
PR	13-SEP-1999;	99US-0153758P.	
PR	15-SEP-1999;	99US-0154018P.	
PR	16-SEP-1999;	99US-0154039P.	
PR	20-SEP-1999;	99US-0154779P.	
PR	22-SEP-1999;	99US-0155139P.	
PR	23-SEP-1999;	99US-0155486P.	
PR	24-SEP-1999;	99US-0155659P.	
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PR	29-SEP-1999;	99US-0156596P.	
PR	04-OCT-1999;	99US-0157117P.	
PR	05-OCT-1999;	99US-0157753P.	
PR	06-OCT-1999;	99US-0157865P.	
PR	07-OCT-1999;	99US-0158029P.	
PR	08-OCT-1999;	99US-0158232P.	
PR	12-OCT-1999;	99US-0158369P.	
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PR	14-OCT-1999;	99US-0159330P.	
PR	14-OCT-1999;	99US-0159331P.	
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PR	21-OCT-1999;	99US-0160815P.	
PR	22-OCT-1999;	99US-0160980P.	
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PR	22-OCT-1999;	99US-0160989P.	
PR	25-OCT-1999;	99US-0161404P.	
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PR	25-OCT-1999;	99US-0161406P.	
PR	26-OCT-1999;	99US-0161359P.	
PR	26-OCT-1999;	99US-0161360P.	
PR	26-OCT-1999;	99US-0161361P.	
PR	28-OCT-1999;	99US-0161920P.	
PR	28-OCT-1999;	99US-0161992P.	
PR	28-OCT-1999;	99US-0161993P.	
PR	29-OCT-1999;	99US-0162142P.	

Query Match

Best Local Similarity 17.5%; Score 342; DB 3; Length 393;

Matches 103; Conservative 50; Mismatches 127; Indels 52; Gaps 10;

QY	24	SSRLQDDRVTPTCHSTSEPRCSRF-----PDGSGSPATWDFGIDWNRIDEPILL 77	
Db	22	SAXMVD-----TSAGEKRLSDVMPPEKVDGGYIGGWNK-----DDGSL- 63	
QY	78	PSIKYKGIPIKISLENVCASQIGKXENEDRDFQAQITDE---VLYPAYVDHGGA 134	
Db	64	-----SCGYCSFRGKRSTMEDFDIKASTIEGQAVCMFGIFDGHGSGRA 107	
QY	135	ADFCHTHMEKIMDLLPKENKLETLTLAFLRIDKAFSHARLSADATLLTSGTTATVAL 194	
Db	108	ABYLKEHLFNNLMKHPQFTDTKLALNETYKQIDVAFLE-----SEKDYRDDGSTASAAV 163	
QY	195	LRDGIELVVASGDSRAILCRKGPKMLTIDHTPERKDEKRIKKGCGFVAMNSLGQPHV 254	

Db	164	L-VGNHLYVANVGDSRTIVSKAGKAIASDDHKPNRSDEKRIESAGGVIMW--AGTWRV 220	
QY	255	NGRLAMTRISGDLDKTSGVTAEPETKRIKLHADDSDLVLTDTGDNFMVNSQICDFVN 314	
Db	221	GGVLAMSAFGNMLK-QFVVAEPEIQDLEIDH-EALLVLASDGLWDVVDNEAVALAQ 278	
QY	315	QCHDPNEAAHAAVTEQAIQYGTEDNSTAVVVPF 346	
Db	279	SEEPERAAARKLTDTAFSRGSADNITCIVVKF 310	
RESULT 42			
AAG39774			
ID	AAG39774 standard; protein; 420 AA.		
XX	AAG39774;		
AC	AAG39774;		
DT	18-OCT-2000 (first entry)		
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 49264.		
DE	Arabidopsis thaliana		
XX	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX	Arabidopsis thaliana.		
XX	EP1033405-A2.		
PN	06-SEP-2000.		
PD	25-FEB-2000; 2000EP-00301439.		
XX	99US-0121825P.		
PR	99US-0123180P.		
PR	99US-0123548P.		
PR	99US-0125788P.		
PR	99US-0126264P.		
PR	99US-0126785P.		
PR	99US-0127462P.		
PR	99US-0128234P.		
PR	99US-0128714P.		
PR	99US-0129845P.		
PR	99US-0130077P.		
PR	99US-0130449P.		
PR	99US-0130510P.		
PR	99US-0130891P.		
PR	99US-0131449P.		
PR	99US-0132048P.		
PR	99US-0132407P.		
PR	99US-0132484P.		
PR	99US-0132485P.		
PR	99US-0132486P.		
PR	99US-0132487P.		
PR	99US-0132863P.		
PR	99US-0134256P.		
PR	99US-0134218P.		
PR	99US-0134219P.		
PR	99US-0134221P.		
PR	99US-0134370P.		
PR	99US-0134768P.		
PR	99US-0134941P.		
PR	99US-0135124P.		
PR	99US-0135353P.		
PR	99US-0135629P.		
PR	99US-0136021P.		
PR	99US-0136392P.		
PR	99US-0136782P.		
PR	99US-0137222P.		
PR	99US-0137528P.		
PR	99US-0137502P.		
PR	99US-0137724P.		
PR	99US-0138094P.		

PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
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PR 22-JUN-1999; 99US-0139817P.
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PR 23-JUN-1999; 99US-0140353P.
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PR 28-JUN-1999; 99US-0140823P.
PR 30-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 02-JUL-1999; 99US-0142544P.
PR 06-JUL-1999; 99US-0142055P.
PR 08-JUL-1999; 99US-0142390P.
PR 09-JUL-1999; 99US-0142803P.
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PR 23-JUL-1999; 99US-0145145P.
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PR 27-JUL-1999; 99US-0145919P.
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PR 05-AUG-1999; 99US-0147192P.
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PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153707P.
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PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 17.5%; Score 342; DB 3; Length 420;

Best Local Similarity 31.0%; Pred. No. 2.8e-28;

Matches 103; Conservative 50; Mismatches 127; Indels 52; Gaps 10;

QY

24 SSRLLQDRRVTPTCHSSTSEPRCSRFD-----PDGSGSPATWDFGWDNRIDEPIIL 77

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Qy      78  PPSIKYKPIKISLENVGCASQIGKREKEDREFDFAQLTDE---VLYFAVYDGHGSPAA 134
Db      101  -----SCGYCSPRGKSTWEDFYDIKASTIEGQAVCMFGIEDGHGSSRA 144
Qy      135  ADPCHTMEKIMDLLEPKKNLETLTLAFLAFLDKAFSSHARLSADATILTSGTATVAL 194
Db      145  AEYLKEHLFNNLMKHPOFLDTKLALNETYKQTVAFLE-----SEKDYRDDGSTASAAV 200
Qy      195  LRDGIELVAVSGVDSRAILCRKQPKMLTIDHTPERKDEKERIKKCGGFVAVNSLGGPHV 254
Db      201  L-VGNHLYVAVGDSRTIVSKAGRAIALSDHKENRSDERKRIESAGGVIMW--AGTRV 257
Qy      255  NGRILATRSIGDLDLKTSVGAETPKRIKLHADDSEFLVLTDTGINFMVNSQBIQCFVN 314
Db      258  CGVLAMSAFGRNMLK-QFVVAEPIQOLEIDH-EAELLVLASDGLWDVVPNEDAVALAQ 315
Qy      315  QCHDPNEAAHVAVTQALQYGTEDNSTAVVVPF 346
Db      316  SEEPPEAAARKLDTATSRGSADNITCIVVKF 347

RESULT 43
AAG39776
ID  AAG39776 standard; protein; 358 AA.
XX
AC  AAG39776;
XX
DT  18-OCT-2000 (first entry)
XX
DE  Arabidopsis thaliana protein fragment SEQ ID NO: 49266.
XX
KW  Protein identification; signal transduction pathway; metabolic pathway;
KW  hybridisation assay; genetic mapping; gene expression control; promoter;
KW  termination sequence.
XX
OS  Arabidopsis thaliana.
XX
FN  EP1033405-A2.
XX
PD  06-SEP-2000.
XX
XX
PF  25-FEB-2000; 2000EP-00301439.
XX
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PR  05-MAR-1999; 99US-0123180P.
PR  09-MAR-1999; 99US-0123548P.
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PR  29-MAR-1999; 99US-0126785P.
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PR  06-APR-1999; 99US-0128234P.
PR  08-APR-1999; 99US-0128714P.
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PR  19-APR-1999; 99US-0130077P.
PR  21-APR-1999; 99US-0130449P.
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PR  23-APR-1999; 99US-0130891P.
PR  28-APR-1999; 99US-0131449P.
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QY	211	AILCRXGKPMKLTIIDHTPERKDSEKRIKCGGFVAWNSLQOPHVNGRLAMTRSIGDLDLK	270
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XX EP1033405-A2.
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QY	211	AILCRKGMKMLTIDHTPERKDEKERIKKCGGFVAVNSLQPHVNGRLANTRSIGDLDLK 270
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KW	termination sequence.	
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PR	18-JUN-1999;	99US-0139454P.
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Db 60 VAPLRGDANGPP-----PESSSSPATKSSIMI-SSRDPNALLSGGSGISFLAGVTVKF- 111
QY 94 NVGCASQIGKXKXENEDRDFQAQLTD----EVLVAYVDHGHPAADFCFTHMEKCM-- 147
Db 112 SYGSSLKGRATMEDYFE-TRISDVNGQWVAFGVDGHHGGARTAEYLNKNLFLKLVSH 170
QY 148 -DLLPKKNLETLTLTFLAFLBIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASV 206

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Db 171 DDFISDTKK-----AIVRFQOTDEYLTIERAGQPKNAGSTAATALL-IGDKLIVANV 222
Qy 207 GDSRAILCRKQKPKMLTIDHTPRKDKERIKKCGGFVAMNSLGQPHVNGRLAMTRSIGD 266
Db 223 GDSRVASRNGSAVPLSDHDKPDSRDERQIEDAGGFLIW--AGTWVGGILAVSRAFGD 280
Qy 267 LDLKTSVVIAPETPKRIKLHADDSTFVLVTDGINFVNSQIECDFVNCQCHDNEAAHAV 326
Db 281 KQLKPY-VIAPETQEBDISTLE--FIVVASDGLWNLNKDAVAIVRDISDAETNAIKL 337
Qy 327 TEQAIQYQGTEDNSTAVVVPF 346
Db 338 VQEGYARGSCDNITCIVRP 357
RESULT 48
AAE01344
ID AAE01344 standard; protein; 434 AA.
AC AAE01344;
XX
DT 31-JUL-2001 (first entry)
DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 1, ABI1 protein.
KW Abscisic acid; ABA; ABA-insensitive; ABI1; signal transduction;
KW kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;
KW tomato; pine; soybean; peanut; olive.
XX
OS Arabidopsis thaliana.
XX
PN WO200136596-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-US031739.
XX
PR 17-NOV-1999; 99US-0166080P.
XX
PA (PTON-) PIONEER HI-BRED INT INC.
XX
PI Helentjaris T;
XX
DR WPI; 2001-329218/34.
DR N-PSDB; AAD05660.
XX
XX DNA constructs containing an abscisic acid-associated sequence are used
PT to modulate a response in a plant to abscisic acid so that the plants are
PT protected against any harmful or detrimental effects of stress and
PT environmental conditions.
XX
PS Claim 3; Page 46; 60pp; English.
XX
CC The invention relates to a method for modulating a response in a target
CC plant to abscisic acid (ABA) by introducing a DNA construct comprising an
CC ABA-associated sequence operably linked to an early kernel/embryo
CC promoter into the plant. The method also involves modulating ABA
CC perception and signal transduction in developing seeds. The method is
CC used to produce plants, particularly cereal plants such as maize, which
CC have a modified response to ABA so that an increase in yield can be
CC produced. The plants are protected against any harmful/detrimental
CC effects of stress and adverse environmental conditions. The ABA function
CC is disrupted in a tissue and developmental preferred manner so that
CC female reproductive tissue is insulated from the stress or adverse
CC environmental conditions. Other plants which can be transformed include
CC rice, cotton, citrus trees, tomatoes, pines, soybean, peanut and olive.
CC The present sequence is Arabidopsis thaliana ABA-insensitive 1 (ABI1)
CC protein
XX
SQ Sequence 434 AA;
Query Match 17.3%; Score 338; DB 4; Length 434;

Best Local Similarity 30.9%; Pred. No. 8.1e-28;
Matches 100; Conservative 46; Mismatches 98; Indels 80; Gaps 12;
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Db 130 GFTSICGRPEMEDAVSTIPRFLOQSSSGMLDGRFDPQSAAH---FFGVYDGHGSGQVAN 186
Qy 137 FCHTHMKECIVDLLPKENL-----ETLLTLAPLEIDKAFSSHARLSADATLLT 185
Db 187 YCRRHMLAAEIAEKPKMLCDGTWLEKWKXKALFNSFLRVDSIESVAP-----ET 239
Qy 186 SGTATVALLRDIIELVVASVGSRAILCRKQKPKMLTIDHTPERKDKERIKKCGG-FV 244
Db 240 VGSTSVAVVPPS-HIFVANCDSRAVLRCRGKTALPLSVHDKPKPDEEAARIEAAGKVI 298
Qy 245 ANNSLGQPHVNGRLAMTRSIGDLDLKTSGVTAEP-----TKRIKLHADDSTFVLVTDGIN 301
Db 299 QWNG---ARVFGVLWRSRISGRYLKPS-IIPDPEVAVKRVK---EDDCILIASDGVW 350
Qy 302 FMVNSQIECDFVQ-----CHDPN-----EAAHAVTEQAIQV 334
Db 351 DVMTDEEACEAVARKILLWHKKNVAGDASLLADERRRKEGKDPAAVSAAYLSKLAIORG 410
Qy 335 TEDNSTAVVVPFGAWGKYKNSIN 358
Db 411 SKDNISVVVVVDLKRPRKLSKPLN 434
RESULT 49
AAE36344
ID AAE36344 standard; protein; 434 AA.
XX
AC AAE36344;
XX
DT 26-JUN-2003 (first entry)
DE Arabidopsis thaliana LMP encoded by pk105 cDNA clone.
XX
XX Lipid metabolism protein; LMP; seed storage; transgenic; plant; cress.
XX Arabidopsis thaliana.
XX
PN WO200299076-A2.
XX
PD 12-DEC-2002.
XX
PF 04-JUN-2002; 2002WO-US017937.
XX
PR 04-JUN-2001; 2001US-0295680P.
XX
XX (BADI) BASF PLANT SCI GMBH.
XX
PI Mittendorf V, Haertel H, Cirpus P;
XX
DR WPI; 2003-140611/13.
DR N-PSDB; AAD54922.
XX
XX New isolated lipid metabolism protein (LMP) nucleic acids and proteins
PT modulating seed storage compound in a plant, useful for producing
PT transgenic plants with modified or increased lipids, fatty acids,
PT cofactors and enzymes.
XX
PS Claim 2; Fig 22B; 52pp; English.
XX
CC The invention relates to lipid metabolism protein (LMP) nucleic acids and
CC proteins modulating seed storage compound in a plant. The invention also
CC relates to a method for producing a transgenic plant having a modified
CC level of a seed storage compound, which involves transforming a plant
CC cell with an expression vector having LMP. The method is useful for
CC modifying or increasing lipids and fatty acids, cofactors and enzymes in
CC transgenic plants. The present sequence is Arabidopsis thaliana LMP
CC protein
XX

SQ Sequence 434 AA;
 Query Match 17.3%; Score 338; DB 6; Length 434;
 Best Local Similarity 30.9%; Pred. No. 8.1e-28;
 Matches 100; Conservative 46; Mismatches 98; Indels 80; Gaps 12;

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 DB 130 GFTSICGRPEMEDAVSTIPRFLOSSSGSMLDGRFPQSAAH---FFGVYDGHGGSQVAN 186
 QY 137 FCHTHMEKCIIMDLIPKKNL-----ETLLTLAFLEIDKAFSSSHARLSADATLLT 185
 DB 187 YCREMHLALAEIAKEKPMLCDGDTWLEKWKALFNSFLRVDSIESVAP-----ET 239
 QY 186 SGTATVALLRDGIELVVASVGSRAILCRKPKMLTIDHTPERKDEKERIKKCGG-FV 244
 DB 240 VGSTSVAVVFPF-HIFVANCSDSRAVLCRGKTALPLSDHDKFDEDEAARIEAAGKVI 298
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RESULT 50
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 ID AAE01348 standard; protein; 434 AA.
 XX AAE01348;
 AC AAE01348;
 XX 31-JUL-2001 (first entry)
 DT Arabidopsis thaliana ABA (abscisic acid)-insensitive 1, abil mutant.
 DE Arabidopsis thaliana ABA (abscisic acid)-insensitive 1, abil mutant.
 XX Abscisic acid; ABA; ABA-insensitive, abil; signal transduction;
 XX kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;
 KW tomato; pine; soybean; peanut; olive; mutant; mutein.
 XX Arabidopsis thaliana.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 180
 FT /notes= "Wild type Gly substituted with Asp"
 FT
 XX WO200136596-A2.
 XX
 XX 25-MAY-2001.
 XX
 XX 17-NOV-2000; 2000WO-US031739.
 XX
 XX 17-NOV-1999; 99US-0166080P.
 XX
 XX (PION-) PIONEER HI-BRED INT INC.
 XX
 XX Helentjaris T;
 XX
 XX WPI; 2001-329218/34.
 DR N-PSDB; AAD05667.
 DR
 XX DNA constructs containing an abscisic acid-associated sequence are used
 PT to modulate a response in a plant to abscisic acid so that the plants are
 PT protected against any harmful or detrimental effects of stress and
 PT environmental conditions.
 XX
 XX Claim 5; Page; 60pp; English.
 PS
 XX

CC The invention relates to a method for modulating a response in a target
 CC plant to abscisic acid (ABA) by introducing a DNA construct comprising an
 CC ABA-associated sequence operably linked to an early kernel/embryo
 CC promoter into the plant. The method also involves modulating ABA
 CC perception and signal transduction in developing seeds. The method is
 CC used to produce plants, particularly cereal plants such as maize, which
 CC have a modified response to ABA so that an increase in yield can be
 CC produced. The plants are protected against any harmful/detrimental
 CC effects of stress and adverse environmental conditions. The ABA function
 CC is disrupted in a tissue and developmental preferred manner so that
 CC female reproductive tissue is insulated from the stress or adverse
 CC environmental conditions. Other plants which can be transformed include
 CC rice, cotton, citrus trees, tomatoes, pines, soybean, peanut and olive.
 CC The present sequence is a Arabidopsis thaliana ABA-insensitive 1 (abil)
 CC mutant. Note: The present sequence is not shown in the specification but
 CC is derived from ABII protein referred as SED ID NO: 4 (AAE01344) and
 CC shown in sequence listing of the specification
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SQ Sequence 434 AA;

Query Match 17.0%; Score 331; DB 4; Length 434;
 Best Local Similarity 30.6%; Pred. No. 4.8e-27;
 Matches 99; Conservative 46; Mismatches 99; Indels 80; Gaps 12;

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 DB 130 GFTSICGRPEMEDAVSTIPRFLOSSSGSMLDGRFPQSAAH---FFGVYDGHGGSQVAN 186
 QY 137 FCHTHMEKCIIMDLIPKKNL-----ETLLTLAFLEIDKAFSSSHARLSADATLLT 185
 DB 187 YCREMHLALAEIAKEKPMLCDGDTWLEKWKALFNSFLRVDSIESVAP-----ET 239
 QY 186 SGTATVALLRDGIELVVASVGSRAILCRKPKMLTIDHTPERKDEKERIKKCGG-FV 244
 DB 240 VGSTSVAVVFPF-HIFVANCSDSRAVLCRGKTALPLSDHDKFDEDEAARIEAAGKVI 298
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 DB 299 QWNG---ARVFGVLAMSRISGLRYLXPS-IIPPEVTAVKRVK-----EDDCILASDGVW 350
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 DB 351 DVMTDEACEWARKRIILLWHKKNVAGDASLLADERKKEGKOPAAVSAAYLSKLAIQRG 410
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OM protein - protein search, using sw model

Run on: October 17, 2004, 15:21:58 ; Search time 93 Seconds
(without alignments)

1287.197 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951

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Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters:

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Maximum DB seq	length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed; and is derived by analysis of the total score distribution.

SUMMARIES

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5	1951	100.0	372	9	US-09-973-964-4		Sequence 4, Appli
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7	1951	100.0	372	9	US-09-972-084-4		Sequence 4, Appli
8	1951	100.0	372	9	US-09-972-785-4		Sequence 4, Appli
9	1951	100.0	372	9	US-09-973-965-4		Sequence 4, Appli
10	1951	100.0	372	9	US-09-973-941-4		Sequence 2, Appli
11	1951	100.0	372	10	US-09-986-992-2		Sequence 1, Appli
12	1951	100.0	372	10	US-09-971-782-4		Sequence 1, Appli
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14	1951	100.0	372	16	US-10-716-488-2		Sequence 2, Appli
15	1951	100.0	372	16	US-10-716-489-2		Sequence 2, Appli

ALIGNMENTS

RESULT 1

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; Sequence 4, Application US/09973963
; Patent No. US20020106676A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-MarC
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen

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;; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative

;; FILE REFERENCE: Diseases

;; CURRENT APPLICATION NUMBER: US/09/973,963

;; PRIOR FILING DATE: 2001-10-11

;; PRIOR FILING DATE: 2000-10-17

;; PRIOR FILING DATE: 2000-10-17

;; PRIOR FILING DATE: 2001-07-13

;; NUMBER OF SEQ ID NOS: 8

;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 4

;; LENGTH: 372

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; US-09-973-963-4

Query Match 100.0%; Score 1951; DB 9; Length 372;

Best Local Similarity 100.0%; Pred. No. 4.3e-205;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRDPDGGSGSPAT 60
DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRDPDGGSGSPAT 60
QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
QY 121 LYFAVDYDGHGPGAAADFCHTHMEKIMDLPKPKNLTLLTFLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVDYDGHGPGAAADFCHTHMEKIMDLPKPKNLTLLTFLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDTKTSQVIAEPETKRIKLHADDPSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDTKTSQVIAEPETKRIKLHADDPSFLVLTDDGI 300
QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVPPFGANGKYKNSINFS 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVPPFGANGKYKNSINFS 360
QY 361 FRSFASGRWA 372
DB 361 FRSFASGRWA 372
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RESULT 2

US-09-973-064-4

;; Sequence 4, Application US/09973064

;; Patent No. US2002010673A1

;; GENERAL INFORMATION:

;; APPLICANT: Roch, Jean-Marc

;; APPLICANT: Bartel, Paul L.

;; APPLICANT: Heichman, Karen

;; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative

;; FILE REFERENCE: Diseases

;; CURRENT APPLICATION NUMBER: US/09/973,064

;; PRIOR FILING DATE: 2001-10-10

;; PRIOR FILING DATE: 2000-10-17

;; NUMBER OF SEQ ID NOS: 4

;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 4

;; LENGTH: 372

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; US-09-973-064-4

Query Match

Best Local Similarity 100.0%; Score 1951; DB 9; Length 372;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRDPDGGSGSPAT 60
QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
QY 121 LYFAVDYDGHGPGAAADFCHTHMEKIMDLPKPKNLTLLTFLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVDYDGHGPGAAADFCHTHMEKIMDLPKPKNLTLLTFLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
DB 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDTKTSQVIAEPETKRIKLHADDPSFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLDTKTSQVIAEPETKRIKLHADDPSFLVLTDDGI 300
QY 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVPPFGANGKYKNSINFS 360
DB 301 NFMVNSQEICDFVNOCHDPNEAAHVAHQIAOYGTEDNSTAVVPPFGANGKYKNSINFS 360
QY 361 FRSFASGRWA 372
DB 361 FRSFASGRWA 372
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RESULT 3

US-09-973-077-4

;; Sequence 4, Application US/09973077

;; Patent No. US20020114799A1

;; GENERAL INFORMATION:

;; APPLICANT: Roch, Jean-Marc

;; APPLICANT: Bartel, Paul L.

;; APPLICANT: Heichman, Karen

;; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative

;; FILE REFERENCE: Diseases

;; CURRENT APPLICATION NUMBER: US/09/973,077

;; PRIOR FILING DATE: 2001-10-10

;; PRIOR FILING DATE: 2000-10-17

;; NUMBER OF SEQ ID NOS: 4

;; SOFTWARE: Patent In Ver. 2.0

;; SEQ ID NO 4

;; LENGTH: 372

;; TYPE: PRT

;; ORGANISM: Homo sapiens

;; US-09-973-077-4

Query Match

Best Local Similarity 100.0%; Score 1951; DB 9; Length 372;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSTAALITLVRSQGNQVRRVLLSSRLQDDRRVPTCHSSTSEPRCSRDPDGGSGSPAT 60
QY 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
DB 61 WDNFGIWNDRIDEPILLPPSIKYGKPIKISLENVGCASQIGRKENEDRFDFAQLTDEV 120
QY 121 LYFAVDYDGHGPGAAADFCHTHMEKIMDLPKPKNLTLLTFLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVDYDGHGPGAAADFCHTHMEKIMDLPKPKNLTLLTFLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPMKLTIDHTPERKDEKERIKK 240
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Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDTKSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDTKSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Qy 301 NFMVNSQICDFVNOCHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 301 NFMVNSQICDFVNOCHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 4

US-09-973-063-4
; Sequence 4, Application US/09973063
; Patent No. US20020115119A1
; GENERAL INFORMATION:

; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,063
; PRIOR FILING DATE: 2001-10-10
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-063-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205; Indels 0; Gaps 0;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGPAT 60
Db 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGPAT 60
Qy 61 WDNFGIWDNRIDEPTLLPSPKIPKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPTLLPSPKIPKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
Qy 121 LYFAYVDGHHGPPAAADFCHTHMEKIMDLPKKNLETLTLLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDGHHGPPAAADFCHTHMEKIMDLPKKNLETLTLLAFLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDTKSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDTKSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Qy 301 NFMVNSQICDFVNOCHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 301 NFMVNSQICDFVNOCHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 5

US-09-973-964-4
; Sequence 4, Application US/09973964
; Patent No. US20020115606A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,964
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-964-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205; Indels 0; Gaps 0;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGPAT 60
Db 1 MSTAALITLVRSGNQVRRVLLSSRLQDDRRVTPTCHSSTSEPRCSRFPDGGSGPAT 60
Qy 61 WDNFGIWDNRIDEPTLLPSPKIPKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPTLLPSPKIPKISLENVGCASQIGKREKEDRDFPAQLTDEV 120
Qy 121 LYFAYVDGHHGPPAAADFCHTHMEKIMDLPKKNLETLTLLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDGHHGPPAAADFCHTHMEKIMDLPKKNLETLTLLAFLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
Qy 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDTKSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Db 241 GGFVAVNSLGQPHVNGRLAMTRISIGDLDTKSGVIAEPETKRIKLHADDSEFLVLTDDGI 300
Qy 301 NFMVNSQICDFVNOCHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 301 NFMVNSQICDFVNOCHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Qy 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 6

US-09-975-072-4
; Sequence 4, Application US/09975072
; Patent No. US20020115607A1
; GENERAL INFORMATION:

; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/975,072
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-072-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSTAALITLVRS	GNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT	60
DB	1	MSTAALITLVRS	GNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT	60
QY	61	WDFGWDNRIDEP	ILLPPSIKYGKPIPKISLENVGCASQIGKRKENE	120
DB	61	WDFGWDNRIDEP	ILLPPSIKYGKPIPKISLENVGCASQIGKRKENE	120
QY	121	LYFAVDG	HGGPAAADFC	180
DB	121	LYFAVDG	HGGPAAADFC	180
QY	181	ATLTS	GTATVALLRDGIELVVASV	240
DB	181	ATLTS	GTATVALLRDGIELVVASV	240
QY	241	GGFVAMNS	LGOPHVNGLAMTRISIGDLKTS	300
DB	241	GGFVAMNS	LGOPHVNGLAMTRISIGDLKTS	300
QY	301	NFMVNS	OEICDFVNQCHDPNEAAH	360
DB	301	NFMVNS	OEICDFVNQCHDPNEAAH	360
QY	361	FSRSF	ASSGRWA	372
DB	361	FSRSF	ASSGRWA	372

RESULT 7

US-09-972-038-4
; Sequence 4, Application US/09972038
; Patent No. US20020119155A1
; GENERAL INFORMATION:

; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,038
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-038-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSTAALITLVRS	GNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT	60
DB	1	MSTAALITLVRS	GNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT	60
QY	61	WDFGWDNRIDEP	ILLPPSIKYGKPIPKISLENVGCASQIGKRKENE	120

DB	61	WDFGWDNRIDEP	ILLPPSIKYGKPIPKISLENVGCASQIGKRKENE	120
QY	121	LYFAVDG	HGGPAAADFC	180
DB	121	LYFAVDG	HGGPAAADFC	180
QY	181	ATLTS	GTATVALLRDGIELVVASV	240
DB	181	ATLTS	GTATVALLRDGIELVVASV	240
QY	241	GGFVAMNS	LGOPHVNGLAMTRISIGDLKTS	300
DB	241	GGFVAMNS	LGOPHVNGLAMTRISIGDLKTS	300
QY	301	NFMVNS	OEICDFVNQCHDPNEAAH	360
DB	301	NFMVNS	OEICDFVNQCHDPNEAAH	360
QY	361	FSRSF	ASSGRWA	372
DB	361	FSRSF	ASSGRWA	372

RESULT 8

US-09-972-757-4
; Sequence 4, Application US/09972757
; Patent No. US2002011927A1
; GENERAL INFORMATION:

; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/972,757
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-757-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSTAALITLVRS	GNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT	60
DB	1	MSTAALITLVRS	GNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSPAT	60
QY	61	WDFGWDNRIDEP	ILLPPSIKYGKPIPKISLENVGCASQIGKRKENE	120
DB	61	WDFGWDNRIDEP	ILLPPSIKYGKPIPKISLENVGCASQIGKRKENE	120
QY	121	LYFAVDG	HGGPAAADFC	180
DB	121	LYFAVDG	HGGPAAADFC	180
QY	181	ATLTS	GTATVALLRDGIELVVASV	240
DB	181	ATLTS	GTATVALLRDGIELVVASV	240
QY	241	GGFVAMNS	LGOPHVNGLAMTRISIGDLKTS	300
DB	241	GGFVAMNS	LGOPHVNGLAMTRISIGDLKTS	300
QY	301	NFMVNS	OEICDFVNQCHDPNEAAH	360
DB	301	NFMVNS	OEICDFVNQCHDPNEAAH	360

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QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 9
US-09-973-965-4
; Sequence 4, Application US/09973965
; Patent No. US20020124273A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,965
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-965-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 60
Db 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 60
QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
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Db 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLLTFLAFLKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKPKMLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKPKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 300
Db 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 300
QY 301 NFMVNSQICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVVPFGAWGKYKNSINF 360
Db 301 NFMVNSQICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVVPFGAWGKYKNSINF 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 10
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US2002016465A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
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; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,941
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-941-4

Query Match 100.0%; Score 1951; DB 9; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 60
Db 1 MSTAALITLVRSGNQVRRVLLSRLLQDDRRVPTCHSSTSEPRCSRFPDGGSGPAT 60
QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
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Db 121 LYFAVYDGHGGPAAADFCHTHMEKICIMDLLPKENLETLLTFLAFLKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKPKMLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKPKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 300
Db 241 GGFVAVNSLQGVHNGRLAMTRISIGDLTKTSGVIAEPETKRIKLHADDSPFLVLTDDGI 300
QY 301 NFMVNSQICDFVNOCHDPNEAAHVAHQIYGTEDNSTAVVVPFGAWGKYKNSINF 360
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QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 11
US-09-986-992-2
; Sequence 2, Application US/09986992
; Publication No. US20030027308A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; FILE REFERENCE: GENOMIC SEQUENCING
; FILE REFERENCE: 038602/1277
; CURRENT APPLICATION NUMBER: US/09/986,992
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/246,974
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: 60/208,291
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-992-2
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Query Match 100.0%; Score 1951; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDRLRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDRLRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKNEDEDRFPAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKNEDEDRFPAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180

QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300

QY 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGANGKYKNSINF 360
DB 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGANGKYKNSINF 360

QY 361 FSRSFASSGRWA 372
DB 361 FSRSFASSGRWA 372

RESULT 12
US-09-371-782-4
; Sequence 4, Application US/09971782
; Publication No. US20030186317A1
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; TITLE OF INVENTION: Diseases
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/971,782
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-371-782-4

Query Match 100.0%; Score 1951; DB 10; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDRLRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDRLRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKNEDEDRFPAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKNEDEDRFPAQLTDEV 120

QY 121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180
DB 121 LYFAVVDGHHGGAADFCFTHMEKCIIMDLPEKKNLETLTLLAFLEIDKAFSSHARLSAD 180
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QY 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
DB 181 ATLLTSGTTATVALLRDGIELVVASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

QY 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300
DB 241 GGFVAMNSLGQPHVNGRLAMTRSIGDLKTSQVIAEPETKRIKLHADDSPFLVLTDDGI 300

QY 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGANGKYKNSINF 360
DB 301 NFMVNSQIEICDFVNOCHDPNEAAHVAHQAIQVGTEDNSTAVVVPFGANGKYKNSINF 360

QY 361 FSRSFASSGRWA 372
DB 361 FSRSFASSGRWA 372

RESULT 13
US-10-311-764-1
; Sequence 1, Application US/10311764
; Publication No. US20040023245A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.; AU-YOUNG, Janice K.
; APPLICANT: BAUGHN, Marian R.; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; GANDHI, Ameena R.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: KEARNEY, Liam; LEE, Ernestine A.
; APPLICANT: LU, Yan; NGUYEN, Dannie B.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Javalaxmi
; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.
; APPLICANT: STEWART, Elizabeth A.; TANG, Y. Tom
; APPLICANT: THORNTON, Michael B.; TRIBOULEY, Catherine M.
; APPLICANT: CHAWLA, Narinder K.; YANG, Junming
; APPLICANT: YAO, Monique G.; YUE, Henry
; TITLE OF INVENTION: PROTEIN PHOSPHATASES
; FILE REFERENCE: PI-0126 USN
; CURRENT APPLICATION NUMBER: US/10/311,764
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/US01/19442
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/212,447
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: US 60/213,746
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: US 60/215,210
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/216,529
; PRIOR FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: US 60/218,080
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/220,117
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20040023245A1 8124196CDI
US-10-311-764-1

Query Match 100.0%; Score 1951; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGNQVRRVLLSSRLQDRLRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60
DB 1 MSTAALITLVRSGNQVRRVLLSSRLQDRLRRVPTCHSSTSEPRCSRFPDGGSGSPAT 60

QY 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKNEDEDRFPAQLTDEV 120
DB 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKNEDEDRFPAQLTDEV 120
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Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
Qy 121 LYFAYVDHGPGAAADFCHTHMEKIMDLPKKNLETLTLAPLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDHGPGAAADFCHTHMEKIMDLPKKNLETLTLAPLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDLGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDLGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGLVIAEPETKRIKLHADDSDFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGLVIAEPETKRIKLHADDSDFLVLTDDGI 300
Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FRSFASSGRWA 372
Db 361 FRSFASSGRWA 372

RESULT 14
US-10-716-488-2
; Sequence 2, Application US/10716488
; Publication No. US20040132155A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; FILE REFERENCE: 038602/1277
; CURRENT APPLICATION NUMBER: US/10/716,488
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2000-11-13
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-716-488-2

Query Match 100.0%; Score 1951; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDFPDGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDFPDGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
Qy 121 LYFAYVDHGPGAAADFCHTHMEKIMDLPKKNLETLTLAPLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDHGPGAAADFCHTHMEKIMDLPKKNLETLTLAPLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDLGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDLGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGLVIAEPETKRIKLHADDSDFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGLVIAEPETKRIKLHADDSDFLVLTDDGI 300
Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FRSFASSGRWA 372
Db 361 FRSFASSGRWA 372

RESULT 16
US-10-094-749-1699
; Sequence 1699, Application US/10094749
```

```
Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FRSFASSGRWA 372
Db 361 FRSFASSGRWA 372

RESULT 15
US-10-716-489-2
; Sequence 2, Application US/10716489
; Publication No. US20040157306A1
; GENERAL INFORMATION:
; APPLICANT: FLOWMAN, GREGORY D.
; APPLICANT: WHYTE, DAVID
; APPLICANT: MANNING, GERARD
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
; FILE REFERENCE: 038602/1277
; CURRENT APPLICATION NUMBER: US/10/716,489
; CURRENT FILING DATE: 2003-11-20
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2000-11-13
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-716-489-2

Query Match 100.0%; Score 1951; DB 16; Length 372;
Best Local Similarity 100.0%; Pred. No. 4.3e-205;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDFPDGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDFPDGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
Qy 121 LYFAYVDHGPGAAADFCHTHMEKIMDLPKKNLETLTLAPLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDHGPGAAADFCHTHMEKIMDLPKKNLETLTLAPLEIDKAFSSHARLSAD 180
Qy 181 ATLLTSGTTATVALLRDLGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDLGIELVWASVGDRAILCRKPKMKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGLVIAEPETKRIKLHADDSDFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSGLVIAEPETKRIKLHADDSDFLVLTDDGI 300
Qy 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Db 301 NFMVNSQEICDFVNOCHDPNEAAHVAVTEQAIOYGTEDNSTAVVVPFGAWGKYKNSINFS 360
Qy 361 FRSFASSGRWA 372
Db 361 FRSFASSGRWA 372

RESULT 16
US-10-094-749-1699
; Sequence 1699, Application US/10094749
```

/ Publication No. US20030219741A1

/ GENERAL INFORMATION:

/ APPLICANT: ISOGAI, TAKAO

/ APPLICANT: SUGIYAMA, TOMOYASU

/ APPLICANT: OTSUKI, TEISUJI

/ APPLICANT: WAKAMATSU, AI

/ APPLICANT: SATO, HIROYUKI

/ APPLICANT: ISHII, SHIZUKO

/ APPLICANT: YAMAMOTO, JUN-ICHI

/ APPLICANT: ISONO, YUUKO

/ APPLICANT: HIO, YURI

/ APPLICANT: OTSUKA, KAORU

/ APPLICANT: NAGAI, KEIICHI

/ APPLICANT: IRIE, RYOTARO

/ APPLICANT: TAMECHIKI, ICHIRO

/ APPLICANT: SEKI, NAOHICO

/ APPLICANT: YOSHIKAWA, TSUTOMU

/ APPLICANT: OTSUKA, MOTOKYU

/ APPLICANT: NAGAHARI, KENJI

/ APPLICANT: MASUHO, YASUHIKO

/ TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA

/ FILE REFERENCE: 084335/0160

/ CURRENT APPLICATION NUMBER: US/10/094,749

/ PRIOR FILING DATE: 2002-03-12

/ PRIOR APPLICATION NUMBER: 60/350,435

/ PRIOR FILING DATE: 2002-01-24

/ PRIOR APPLICATION NUMBER: JP 2001-328381

/ PRIOR FILING DATE: 2001-09-14

/ NUMBER OF SEQ ID NOS: 3381

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 1699

/ LENGTH: 372

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-10-094-749-1699

Query Match

Best Local Similarity 99.9%; Score 1950; DB 15; Length 372;

Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRLVSSLLQDDRRVPTCHSSTSEPCSRFPDGGSGSPAT 60

Db 1 MSTAALITLVRSQGNQVRRLVSSLLQDDRRVPTCHSSTSEPCSRFPDGGSGSPAT 60

Qy 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Db 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Qy 121 LYFAVYDGHGPGAAADFCHTHMEKIMDLPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180

Db 121 LYFAVYDGHGPGAAADFCHTHMEKIMDLPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVVASVGDGRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Db 181 ATLLTSGTTATVALLRDGIELVVASVGDGRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Qy 241 GGFVANNLSQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSPFLVLTDDGI 300

Db 241 GGFVANNLSQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSPFLVLTDDGI 300

Qy 301 NFVWNSQECDFVNOCHDPNEAAHVAVEQAIOYGTEDNSTAVVVPFGANGKYKNSINFS 360

Db 301 NFVWNSQECDFVNOCHDPNEAAHVAVEQAIOYGTEDNSTAVVVPFGANGKYKNSINFS 360

Qy 361 FSRSPASSGRWA 372

Db 361 FSRSPASSGRWA 372

RESULT 17

US-10-408-765A-2487

/ Sequence 2487, Application US/10408765A

/ Publication No. US20040101874A1

/ GENERAL INFORMATION:

/ APPLICANT: Ghosh, Soumitra S.

/ APPLICANT: Fathy, Eoin D.

/ APPLICANT: Zhang, Bing

/ APPLICANT: Gibson, Bradford W.

/ APPLICANT: Taylor, Steven W.

/ APPLICANT: Glenn, Gary W.

/ APPLICANT: Warnock, Dale E.

/ TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

/ FILE REFERENCE: 660088.465

/ CURRENT APPLICATION NUMBER: US/10/408,765A

/ CURRENT FILING DATE: 2003-04-04

/ NUMBER OF SEQ ID NOS: 3077

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 2487

/ LENGTH: 372

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-10-408-765A-2487

Query Match

Best Local Similarity 99.9%; Score 1950; DB 16; Length 372;

Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRLVSSLLQDDRRVPTCHSSTSEPCSRFPDGGSGSPAT 60

Db 1 MSTAALITLVRSQGNQVRRLVSSLLQDDRRVPTCHSSTSEPCSRFPDGGSGSPAT 60

Qy 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Db 61 WDNFGIWDNRIDEPILLPSIKYKGPDKISLENVGCASQIGKRKENEDRFPDFAQLTDEV 120

Qy 121 LYFAVYDGHGPGAAADFCHTHMEKIMDLPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180

Db 121 LYFAVYDGHGPGAAADFCHTHMEKIMDLPKEKNLETLTLTFLAFLEIDKAFSSHARLSAD 180

Qy 181 ATLLTSGTTATVALLRDGIELVVASVGDGRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Db 181 ATLLTSGTTATVALLRDGIELVVASVGDGRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240

Qy 241 GGFVANNLSQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSPFLVLTDDGI 300

Db 241 GGFVANNLSQPHVNGRLAMTRISIGDLTKTSVIAEPETKRIKLHADDSPFLVLTDDGI 300

Qy 301 NFVWNSQECDFVNOCHDPNEAAHVAVEQAIOYGTEDNSTAVVVPFGANGKYKNSINFS 360

Db 301 NFVWNSQECDFVNOCHDPNEAAHVAVEQAIOYGTEDNSTAVVVPFGANGKYKNSINFS 360

Qy 361 FSRSPASSGRWA 372

Db 361 FSRSPASSGRWA 372

RESULT 18

US-09-925-300-1655

/ Sequence 1655, Application US/09925300

/ Patent No. US20020151681A1

/ GENERAL INFORMATION:

/ APPLICANT: Craig Rosen,

/ APPLICANT: Steve Ruben,

/ TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

/ FILE REFERENCE: PA101

/ CURRENT APPLICATION NUMBER: US/09/925,300

/ CURRENT FILING DATE: 2001-08-10

/ PRIOR APPLICATION NUMBER: PCT/US00/05988

/ PRIOR FILING DATE: 2000-03-08

/ PRIOR APPLICATION NUMBER: 60/124,270

/ PRIOR FILING DATE: 1999-03-12

/ NUMBER OF SEQ ID NOS: 1890

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 1655

/ LENGTH: 373

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (144)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (290)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (325)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-925-300-1655

Query Match 98.6%; Score 1924; DB 9; Length 373;
Best Local Similarity 98.9%; Pred. No. 4e-202;
Matches 368; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 2 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 61
QY 61 WDNFGIWNRIDEPILLPPSIKYGRPIPKISLENVGCASQIGKKEKNEDEDFDFAQLTDEV 120
Db 62 WDNFGIWNRIDEPILLPPSIKYGRPIPKISLENVGCASQIGKKEKNEDEDFDFAQLTDEV 121
QY 121 LYFAYVDHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 180
Db 122 LYFAYVDHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 181
QY 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 240
Db 182 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 241
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 242 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 301
QY 301 NFMVNSQEICDFVNOCHDNEAAHVAHTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360
Db 302 NFMVNSQEICDFVNOCHDNEAAHVAHTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 361
QY 361 FSRSFASSGRWA 372
Db 362 FSRSFASSGRWA 373

RESULT 19
US-09-850-351-2
; Sequence 2, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
; TITLE OF INVENTION: AND USES THEREFOR
; FILE REFERENCE: 38155-20013.00
; CURRENT APPLICATION NUMBER: US/09/860.351
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: US 60/205,260
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-850-351-2
Query Match 88.5%; Score 1727; DB 9; Length 352;

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Best Local Similarity 99.4%; Pred. No. 1.7e-180;
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLQLQDDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWNRIDEPILLPPSIKYGRPIPKISLENVGCASQIGKKEKNEDEDFDFAQLTDEV 120
Db 61 WDNFGIWNRIDEPILLPPSIKYGRPIPKISLENVGCASQIGKKEKNEDEDFDFAQLTDEV 120
QY 121 LYFAYVDHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAYVDHGGAADFCFTHMEKICIMDLPEKKNLETLTLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 240
Db 181 ATLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKC 240
QY 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAMNSLGQPHVNGRLAMTRISIGDLTKTSQVIAEPETKRIKLHHADDSFLVLTDDGI 300
QY 301 NFMVNSQEICDFVNOCHDNEAAHVAHTEQAIQ 332
Db 301 NFMVNSQEICDFVNOCHDNEAAHVAHTEQVTQ 332

RESULT 20
US-10-353-690-44
; Sequence 44, Application US/10353690
; Publication No. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacqueline
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1692, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 8912, 2868,
; TITLE OF INVENTION: 283, 2554, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; FILE REFERENCE: MPI02-018P1RNMNIM
; CURRENT APPLICATION NUMBER: US/10/353,690
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450

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; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-353-690-44

Query Match      88.5%; Score 1727; DB 15; Length 352;
Best Local Similarity 99.4%; Pred. No. 1.7e-180;
Matches 330; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MSTAALITVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFPDGGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKREKENEEDRFDAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKREKENEEDRFDAQLTDEV 120
Qy 121 LYFAVYDGHGGPAAADFCHTHMEKIM 147
Db 121 LYFAVYDGHGGPAAADFCHTHMEKIM 147
Qy 181 ATLLTSGTTATVALLRDGIELVVASVGDSTRALLCRKGKPMKLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSTRALLCRKGKPMKLTIDHTPERKDEKERIKK 240
Qy 241 GGFVANNLSGQPHVNGRLAMTRISIGDLTKTSVIAEPETKIKLHADDSPFLVITDGI 300
Db 241 GGFVANNLSGQPHVNGRLAMTRISIGDLTKTSVIAEPETKIKLHADDSPFLVITDGI 300
Qy 301 NFWNSQETCDFVNOCHDPNEAAHAYTEQAIO 332
Db 301 NFWNSQETCDFVNOCHDPNEAAHAYTEQVTO 332

RESULT 21
US-10-094-749-3238
; Sequence 3238, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKANATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3238
```

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; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-094-749-3238

Query Match      40.5%; Score 790; DB 15; Length 150;
Best Local Similarity 100.0%; Pred. No. 4.3e-78;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITVRSQGNQVRRVLLSSLLQDDRRVPTCHSSSTSEPRCSRFPDGGSGSPAT 60
Qy 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKREKENEEDRFDAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKREKENEEDRFDAQLTDEV 120
Qy 121 LYFAVYDGHGGPAAADFCHTHMEKIM 147
Db 121 LYFAVYDGHGGPAAADFCHTHMEKIM 147

RESULT 22
US-10-072-012-853
; Sequence 853, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zehrusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Basha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
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/ PRIOR APPLICATION NUMBER: 60/265,514
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,517
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,412
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/265,395
/ PRIOR FILING DATE: 2001-01-31
/ PRIOR APPLICATION NUMBER: 60/266,406
/ PRIOR FILING DATE: 2001-02-02
/ PRIOR APPLICATION NUMBER: 60/266,767
/ PRIOR FILING DATE: 2001-02-05
/ PRIOR APPLICATION NUMBER: 60/267,057
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/266,975
/ PRIOR FILING DATE: 2001-02-07
/ PRIOR APPLICATION NUMBER: 60/267,459
/ PRIOR FILING DATE: 2001-02-08
/ Remaining prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 1391
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 854
/ LENGTH: 252
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Protein
/ OTHER INFORMATION: phosphatase 2C Consensus Sequence
US-10-072-012-854

Query Match      20.3%; Score 395.5; DB 12; Length 252;
Best Local Similarity 40.5%; Pred. No. 2.3e-34;
Matches 105; Conservative 41; Mismatches 90; Indels 23; Gaps 9;

QY      94  NVCCASQIGKRNED-----RPDFAQLTDEVLVYFAVDGCHGPPAAADCTHMEK--C 145
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      2  DVGVSVMQGFRRKPMEDAHIAAGKNLNSGGKSGKGFVAFDGHGSGQAATYAGKHELETKLA 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      146  IMDLLPKENKLETLTLTFLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVAS 205
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      62  LRKSFPELDLLENALKEFLE---STDEELRSSAANTDLDSGSTAVVALLR-GNKLIVAN 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      206  VGDRAILCRKGKPMK-LTIHTPEKDKERIKKCGGFVAVNWSLGGPHVNGRLAMTRSI 264
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      118  VGDRAVLCRNGNAIKQLTECHKPNSDEBRRRIEGAGGFVSRNG---RVNGVLAVSRAF 173
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      265  GDLDLK--TSGVIAPETKRIKLHHAADSFLVLTDTGTFNFMVNSQICDFVQ--CHDP 319
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      174  GDELPKGVLPQVTPADPVTSHKITFSE--FLIASDGLMDVLSDQEVVDIVRSLSGDP 232
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      320  NEAAHAAVTQAIQYGTEDN 338
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      233  MEAAEKLVDAIAYGSEDN 251
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 24
US-09-801-267-4
/ Sequence 4, Application US/09801267
/ Publication No. US20020086296A1
/ GENERAL INFORMATION:
/ APPLICANT: Meyers, Rachel A.
/ TITLE OF INVENTION: 26583, A NOVEL SERINE/THREONINE
/ TITLE OF INVENTION: PHOSPHATASE AND USES THEREFOR
/ FILE REFERENCE: 10448-025001
/ CURRENT APPLICATION NUMBER: US/09/801,267
/ CURRENT FILING DATE: 2001-03-06
/ PRIOR APPLICATION NUMBER: US 60/187,454
/ PRIOR FILING DATE: 2000-03-07
/ NUMBER OF SEQ ID NOS: 5
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 300
/ TYPE: PRT

```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence
US-09-801-267-4

Query Match          19.0%; Score 370.5; DB 12; Length 300;
Best Local Similarity 36.1%; Pred. No. 1.7e-31;
Matches 110; Conservative 39; Mismatches 89; Indels 67; Gaps 12;

QY 94 NVGCASQIGKRNEDRF-----DFAQLTDEVLYFAYVDGHPGPAADFCHTHMEKCI 146
Db 2 DVGVSVMQGWKSMEDAHIALKNLSSSGKDSWFFAVFDGHS-QAAYAGKHLHKT 60

QY 147 M---DLLP-----KEKNLETLTLTFLAFLIDKAFSSHARLSADATL-----LTSG 187
Db 61 LAERKSPFEGDPWEMKLSLEDALESFLEAD---TDEELRSAAASAANKVLTKEDLSSG 117

QY 188 TTATVALLRDGIELVVASVGDRAILCRKQKPMK----LTIDHTPERKDEKERIKKCGGF 243
Db 118 STAVVALIR-GNKLYVANVGDSRAVLCRNGNAIKWAVLTEDHKPSNEDERERIEAAGGF 176

QY 244 VAWNSLGQPHVNGRLAMTSIGDLTKTSG-----VIAEPE-TK 281
Db 177 VSRVSNGR--VNGVLAVSRAGDFELKPGSKLGPEESLEANVEYIKSPQLVTAEPDVTIS 234

QY 282 RIKLHHADDSFLVTTDGINFMVNSQEI CDFV-----NOCHDPNEAAHAHTVTEQAIQY 333
Db 235 STDLTDPKDEFLILACDGLMDVVSDQEVVDIVRSELSDGNKSAEDPMEAAEKLVDEAIAR 294

QY 334 GTEDN 338
Db 295 GSEDN 299

RESULT 25
US-10-170-789-35
; Sequence 35, Application US/10170789
; Publication No. US20030180930A1
; GENERAL INFORMATION:
; APPLICANT: Rachel E. Meyers
; APPLICANT: Olandt, Peter J.
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Williamson, Mark
; APPLICANT: Weich, Nadine
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASE, PHOSPHATASE,
; AND PROTEASE FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-191001
; CURRENT APPLICATION NUMBER: US/10/170,789
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: US 09/797,039
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US01/06525
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,061
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: US 09/882,166
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19269
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/212,078
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 09/934,406
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: PCT/US01/26052
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/226,740
; PRIOR FILING DATE: 2000-08-21
; PRIOR APPLICATION NUMBER: US 09/861,801
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16549
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 60/205,508
```

; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437.963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 164347
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_63255C.1.pep
 US-10-437-963-164347

Query Match 18.9%; Score 369; DB 16; Length 348;
 Best Local Similarity 37.5%; Pred. No. 3.2e-31;
 Matches 99; Conservative 48; Mismatches 85; Indels 32; Gaps 11;

QY 96 GCASQIGKRNED----RPDFAQLTDEVLYFAYVDGHHGPPAAADFCCHTMEKICIMDLLP 151
 DB 84 GYASAPKGRASMEFYETRIDGVD-GETIGLFGVFDGHHGARRAEYVKQL---FSNLIK 139
 QY 152 KEK---NLETLLTAFLEID----KAFSSHARLSADATLLTSGTTATVALLRDGIELVVA 204
 DB 140 HPKFTSIDKSAIAETYNHTSEFLKASSHTR-----DAGSTASTAIL-VGDRLLVA 190
 QY 205 SVGDSRALCKRGPMLKTIDHTPERKDEKRIKKCGFVAVNSLGGPHVNGRLAMTRSI 264
 DB 191 NVGSRVAVCGGDAIAVSRRKEDQDSRQRIEDAGGFVW--AGTWVGGVLAVSRAP 248
 QY 265 GDPLKTSVYAEPTKRIKLHADD--FVLTDTGDNFMVNSQEIICDFVNOCHDNEA 322
 DB 249 GDLLK-QYVVADPE--IKEEIVDSLSLEFLILASDGLVDVNSKEAVDWRPIQDPEQA 304
 QY 323 AHAVTEQAIOGTEDNSTAVVVPF 346
 DB 305 AKRLLEAYQYRGSADNTIVVIRF 328

RESULT 27
 US-10-424-599-219801
 ; Sequence 219801, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424.599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 219801
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_40508C.1.pep
 US-10-424-599-219801

Query Match 18.5%; Score 361; DB 12; Length 405;
 Best Local Similarity 31.7%; Pred. No. 3.1e-30;
 Matches 97; Conservative 59; Mismatches 98; Indels 52; Gaps 12;

QY 71 IDEPILLPSIKYKPIPKISLENVGCASQIGKRNEDRDFPAQLTD----- 118
 DB 81 IEESIETATEF---TPNV---RSGCCADIGPRGMD--EHIQIDDLAAHLGFVKHP 132
 QY 119 -EVLYFAYVDGHHGPPAAADFCCHTMEKICIM---DILPKE-----KNLETLLTFLAFLEI 167
 DB 133 MSAFAVAFVFDGHHGPPAAAFVKNAMRLLFEADMLQSDADALFLKLEDSHRAFLGA 192
 QY 168 KDAFSSHARLSADATLLTSGTTATVALLRDGIELVAVSGDSRALCKRGPMLKTIDHT 227
 DB 193 DLALADEQSVSS-----SCGTTALTALVL-GRHLVAVNAGDCRAVLCRGVAVDSQDHR 246
 QY 228 PERKDEKRIKKCGFVAVNSLGGPHVNGRLAMTRISIGDLDLK---TSGVIARPETKR 282
 DB 247 PSYLPERRRVEELGGFI-----DDGLNGYLSVTRALGDWDLKFLPGSASPLIADPDVGV 301
 QY 283 IKLHADDSEFLVLTDTGDNFMVNSQEIICDFV----NOCHDPNEAAHVAHTQAIOGTEDN 338
 DB 302 VTUTE-DDEFLIIGCDGIWDVSSQDAVSFVRRLRRHDDPQOCARELVKALRLHTSDN 360
 QY 339 STAVV 344
 DB 361 LTVIVI 366

RESULT 28
 US-10-424-599-176581
 ; Sequence 176581, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J
 ; APPLICANT: Kovalic, David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424.599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 176581
 ; LENGTH: 374
 ; TYPE: PRT
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(374)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_130470C.1.pep
 US-10-424-599-176581

Query Match 18.5%; Score 360; DB 12; Length 374;
 Best Local Similarity 31.6%; Pred. No. 3.5e-30;
 Matches 101; Conservative 52; Mismatches 107; Indels 60; Gaps 10;
 QY 78 PSIKYKPIPKISLE-----NVGCASQIGKRNEDR 110
 DB 28 PPSYRCKLVHRASLQMTKLSDVSAEPHEVTDCCSDFFPMLRSGACTDIGFRSNMEDA 87
 QY 111 F-----DEA---QLTDEVLYFAYVDGHHGPPAAADFCCHTMEKICIMDLLPKEKLETL 159
 DB 88 YVCVDMFMDYGLKXHDIGPSAFYVFDGHHGKHADFACHLHPKFIVDKDFPDRIERI 147
 QY 160 LTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIE---LVAVSGDSRALCKR 216
 DB 148 VASAFIQADNAFAEACSLDA---ALASGTTALTATVIGSFXCRLLVANAGDCRAVLCRR 204
 QY 217 GKEMKLTIDHTPERKDEKRIKKCGFVAVNSLGGPHVNGRLAMTRISIGD-----LDLKT 271
 DB 205 GKAIEMSRDHKPGCNKEKRIEASG3YV-----DGYLNGQLNVARALGDWHEGMSKSD 259


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QY 90 ISLENYGASQIGKRKENEDRFQALUTDEVLYFAYVDGHHGGAADFCFHTHMEKCIIM-- 147
Db 9 IALKNLNSSSS-GK-----DSWSEFAVFDGHHGGAQAKYAGKHLHKTILAE 53
QY 148 -DLLP-----KEKNLETLTLTFLAFLIDKAFSSHARLSADATL-----LTSGTGA 190
Db 54 RKSFPDGPWEMKLSLEDAKESFLEAD---TDEILRSASAANKVLTKEDLSSGSTA 110
QY 191 TVALRDGIELVVASVGDGRAILCRKGKPMK-----LTIDHTPERKDEKERIKKGGGVAV 246
Db 111 VVALIR-GNKLYVANYVGDGRAVLRCRNGNAIKWAVTLTDEHKPSNEDRERIEAAGGVSVR 169
QY 247 NSLGQPHVNGRLAWTSIGDLDLKTSG-----VIAEPE-TKRIK 284
Db 170 VSNGR--VNGVLAVSRAFGFEUKPSKLGOPESLEANYEYIKSPQOLVTABPDVTSTD 227
QY 285 LHHADDSFLVLTGGINFMVNSQEIFDFV-----NOCHDPNEAA 323
Db 228 LTPDKDEFILACDGLWDVVQCEVVDIVRSELSDGNKSAEDPMEAA 274

RESULT 39
US-10-425-114-72086
; Sequence 72086, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yinua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72086
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4071-007-B3_FLI.pep
US-10-425-114-72086

Query Match 17.9%; Score 348.5; DB 12; Length 408;
Best Local Similarity 32.8%; Pred. No. 7.4e-29;
Matches 102; Conservative 52; Mismatches 94; Indels 63; Gaps 13;

QY 87 IPKISLE-----NV--GCASQIGKRKENED---RFD--FAQLTDEVL 121
Db 64 VPRMGLLEQPDVAFSLSDTMIQQFVPIRSGSFADIGPRRYMEDHIRIDDLSAHLGSLV 123
QY 122 -----YFAYVDGHHGGAADFCFHTHMEKCIIMD--LLPKE-----KNLETLTLTFLA 165
Db 124 CPLPSAFYGVFDGHHGGAQAAAYKRRHMRFLFBESEFPQASQVDEVLESVCURRAFL 183
QY 166 EIDKAFSSHARLSADATLTLTSGTTATVALLRDGIELVVASVGDGRAILCRKGKPMKLTID 225
Db 184 QADLALADDLDIR-----SSGTTALTALV-FGRQLVVANTGDCRAVLCRKGVAMEMSRD 237
QY 226 HTPERKDEKERIKKGGGVAVNSLQPHVNGRLAWTSIGDLDLKTSG-----VIAEPE 279
Db 238 HRANHVEERERVAASGYIE-----DGYLNGVLVSVTRALGDWDWKAFASASALIAEPE 292
QY 280 TKRIKLLHADDSEFLVLTGGINFMVNSQEIFCDFV-----NOCHDPNEAAHVAITEQAIQGT 335
Db 293 FRATLGE-DDEFVWGCDDIWDVMTSQHAVSLVRGLRQHDDPARCARELVMEAKRLET 351
QY 336 EDNSTAVVWFF 346

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QY 148 DLLPKENLETLTAFLEIDKAFSSHARLSADATLTSQTATVALLRDGIELVWASVG 207
Db 150 EDADFPLEKVVTRSFLEIDAEF--ARSCSTESSLSGGTALTALII-FGRSILLVANAG 205
QY 208 DSRAILCRKGPMLTIDHTPERKDEKRIKCGGFVWNSLGGPHVNGRLATRSIGDL 267
Db 206 DCRAVLGRGGAIEMSKDHRRPLOTCKRKRLIESLGGYI-----DDGYLNGQLGVTRALGDW 260
QY 268 DL-----KTSGVIAEPETKRIKLHADDSEFLVLTDTGDNFMVNSQIEICDF-----VNO 315
Db 261 HLOGMKEINGKGPLSAPELKLITL-TKDEFLIIGSDGWDVFRSONAVDFARRLQE 319
QY 316 CHDPNEAAHVTEQAIQYGTEDNSTAVVVPF 346
Db 320 HNDVKQCCKEIVGEAIRKRGATDNLTVVMICF 350
RESULT 43
US-10-425-114-70158
; Sequence 70158, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70158
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73078B07_FLI.pep
US-10-425-114-70158
Query Match 17.8%; Score 346.5; DB 12; Length 360;
Best Local Similarity 31.2%; Pred. No. 1e-28;
Matches 105; Conservative 58; Mismatches 119; Indels 55; Gaps 12;
QY 52 PDGS-----GSPATWDFGWINRDEPILLPS-----IKYKPIPKISL 92
Db 2 PDGYMVCVEEPKDAERFGDPGVVEEPKFFLAQWERCNTTSADPFQKLSNFVPI-- 59
QY 93 ENVGCASOIGKRKENED-----RFDFQAQLTDEVL-YFAVVDGHHGGAADFCHTH 141
Db 60 -RSGDWSDIGGQYMEDTHVCIPDLAKNFGPPLSDNEVSYGVDFDGHGKDAHFVCDN 118
QY 142 MEKCIIMDLLPKENLETLTAFLEIDKAFSSHARLSADATLTSQTATVALLRDGIEL 201
Db 119 LPRMIVEDSDPFLQLEKVVTRSFLEIDAEF--ARSCSTESSLSGGTALTALII-FGRS 174
QY 202 VVASVGDSPAILCRKGPMLTIDHTPERKDEKRIKCGGFVWNSLGGPHVNGRLAMT 261
Db 175 LVANAGDCRAVLRSRGTAVEMSNDRPCSLSEKLRVESLGGYV-----DDGYLNGQLGV 229
QY 262 RSIGDL-----KTSGVI-AEPTETKRIKLHADDSEFLVLTDTGDNFMVNSQIEICDF- 312
Db 230 RALGDWHLEGMKMGAGETGGPLSADPELKWTL-TKDEFLIIGSDGWDVFRSONAVDFARR 288
QY 313 ---VNOCHDPNEAAHVTEQAIQYGTEDNSTAVVVPF 346
Db 289 RKELQEHNDVKLCREIVEEAIRKRGATDNLTVAVVSP 325
RESULT 44
US-10-437-963-157517

; Sequence 157517, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 157517
; LENGTH: 388
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_57080C.1.pep
US-10-437-963-157517
Query Match 17.8%; Score 346.5; DB 16; Length 388;
Best Local Similarity 32.6%; Pred. No. 1.1e-28;
Matches 94; Conservative 55; Mismatches 98; Indels 41; Gaps 10;
QY 82 KYGKPIPKISLNVGCASOIGKRKENED-----RFDFQAQLTDEVL-YFAVVDGHHG 130
Db 84 XSGNFVPI---RSGDWSDIGGQYMEDTHVCITDLAKNFGQSVNDNEAISFYGVDFGHHG 140
QY 131 GPAADPFCHTHMEKCIIMDLLPKENLETLTAFLEIDKAFSSHARLSADATLTSGTTA 190
Db 141 GKDAHFVRDNLPRILIVEDADPFLEKVVTRSFVHADNQFAK-----TTLSGTTA 192
QY 191 TVALLRDGIELVWASVGDSPAILCRKGPMLTIDHTPERKDEKRIKCGGFVWNSLGG 250
Db 193 LTAMI-FGRTLLIANAGDCRAVLRSRGTAVEMSNDRPCSLSEKLRVESLGGYV-----D 246
QY 251 OFHVNGRLATRSIGDL-----KTSG-----VIAEPTETKRIKLHADDSEFLVLTDTGINF 302
Db 247 DGYLNGQLGVTRALGDWHLEGMKMGAGETGGPLSADPELKWTL-TKDEFLIIGSDGWD 305
QY 303 MVNSQIEICDF---VNOCHDPNEAAHVTEQAIQYGTEDNSTAVVVPF 346
Db 306 VFSQNVDFARRLQEHNDVKSCREIVEEAIRKRGATDNLTVAVVSP 353
RESULT 45
US-10-424-599-219869
; Sequence 219869, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 219869
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4056C.1.pep
US-10-424-599-219869

[illegible]

Search completed: October 17, 2004, 15:23:48
Job time : 97 secs

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 67269
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4759-022-G10_FLI.pep
US-10-425-114-67269

Query Match      17.7%; Score 345.5; DB 12; Length 343;
Best Local Similarity 33.0%; Pred. No. 1.2e-28;
Matches 92; Conservative 59; Mismatches 109; Indels 19; Gaps 9;

QY   78 PPSIKYG---KPIKISLE--NVGCASQIGKKKENEDRFDF--AQLTD-EVLYFAYVD 127
     |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB   56 PPALRSARLNRTPIGSRVDGTLNCGYSFGRRASWEDFYDKASKIDDKQINLFGIFD 115

QY   128 GHGGPAAADFCHTHMEKCINDLLPKENLETLLTFLAFIDKAPSSHARLSADATLLTSG 187
     |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB   116 GHGGSRAAEYLKEHLPENLMKHPEFTNTKLAMSETYRKTDSEFLDAER----NTHRDDG 171

QY   188 TTAVALLRDGIELBVASVGDSAILCRKGKPMKLTIDHTPERKDKERIKKCGGFVAWN 247
     |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB   172 STASTAWM-VADHLIYVANVGDSRAVISKAGKATALSEDHKNRSDERNIESAGGIVMW- 229

QY   248 SLQCPHYNGELATRSIGDLDTKTSGVIAEPETKRILKHAADSFLVLTTDGINFMVNSQ 307
     |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB   230 -AGTWRVGGVLANSRAPGNLLK-QFVIADPEIQEQEINE-ELEFLIIASDGLNDVVVSNE 286

QY   308 EICDFVNQCDDPNEAAHAVTEQAIOYGTEDNSTAVVVPF 346
     :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB   287 DAVTLVKMBEEPEAARKLTETAFRSGSGDNITCIVVKF 325


RESULT 49
US-10-424-599-226401
; Sequence 226401, Application US/10424599
; Publication No. US2004003107A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 226401
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_4646C.1.pep
US-10-424-599-226401

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	Query Match	17.6%; Score 344; DB 12; Length 338;
	Best Local Similarity	35.6%; Pred. No. 1.7e-28;
	Matches	Conservative 49; Mismatches 89; Indels 32; Gaps 10;
Qy	96 GCAGCIGKRNENRFD--FQAQLTDEVL-YFAVVDGCGGPAAADFCHTHMEKCIMDLPLPK	152
Dd	: : : : : : : :	
81	GYASSPGKRSSMEDFYETKDGVGEIVGLGFVDFGHGGAARAEYVKQNL---FSNLTISH	137
Qy	153 EKNLETLTLTAFLIEDKAFFSSHARLSADATLLTS-----GGTTATVALLRDGIELVA	204
Dd	: : : : : : : :	
138	PK-----FISDTKSAIDAYNHTDSFEKSENQNRRDAGSTASTAIL-VGDRLIVA	187
Qy	205 SVGPSRAILCRKGPMKLTI DHTPERKDEKERIKKCGGFVAWNSLQGHVNYGRLAMTRSI	264
Dd	: : : : : : : :	
188	NVGDSRAVICRGNAIAVSRRHKPDOTERRIEDPAGGFVMW---AGTWRVGGVLAVSRAF	245

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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 105 Seconds
(without alignments)
182.903 Million cell updates/sec

Title: US-10-716-488-2
Perfect score: 1951
Sequence: 1 MSTAALITLVRSQGNQVRR.....KNSINFSRSPASSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1951	100.0	372	4	US-09-973-963-4
2	325	16.7	281	2	US-08-822-701-9
3	325	16.7	281	3	US-08-935-855-9
4	319.5	16.4	390	2	US-08-873-093-3
5	319.5	16.4	390	4	US-09-206-646-3
6	314	16.1	392	3	US-09-013-881-2
7	314	16.1	392	4	US-09-612-473-2
8	307.5	15.8	390	4	US-09-206-646-4
9	306.5	15.7	306	2	US-08-822-701-8
10	306.5	15.7	306	3	US-08-935-855-8
11	300	15.4	309	2	US-08-822-701-7
12	300	15.4	309	3	US-08-935-855-7
13	282.5	14.5	478	2	US-08-873-093-1
14	282.5	14.5	478	2	US-08-873-093-4
15	282.5	14.5	479	4	US-09-206-646-1
16	281.5	14.4	387	4	US-09-461-325-178
17	281.5	14.4	387	4	US-10-012-542-178
18	279	14.3	314	2	US-08-822-701-10
19	279	14.3	314	3	US-08-935-855-10
20	228.5	11.7	542	3	US-08-935-855-20
21	226	11.6	546	3	US-08-935-855-20
22	223	11.4	392	2	US-08-822-701-2
23	223	11.4	392	3	US-08-935-855-2
24	197.5	10.1	1874	4	US-09-331-403-2
25	176.5	9.0	504	2	US-08-752-891-6
26	176.5	9.0	504	2	US-09-144-178-6
27	176.5	9.0	504	3	US-09-406-854-6

28	170.5	8.7	504	2	US-08-752-891-2	Sequence 2, Appli
29	170.5	8.7	504	2	US-09-144-178-2	Sequence 2, Appli
30	170.5	8.7	504	3	US-09-406-854-2	Sequence 2, Appli
31	170.5	8.7	504	4	US-09-529-279-2	Sequence 2, Appli
32	170.5	8.7	504	4	US-10-158-895-2	Sequence 2, Appli
33	170.5	8.7	513	4	US-09-529-279-43	Sequence 43, Appli
34	170.5	8.7	513	4	US-10-158-895-43	Sequence 43, Appli
35	170.5	8.7	517	4	US-09-529-279-11	Sequence 11, Appli
36	170.5	8.7	517	4	US-10-158-895-11	Sequence 11, Appli
37	152.5	7.8	251	37	US-09-134-000C-4701	Sequence 4701, Ap
38	149.5	7.7	249	4	US-09-107-532A-6748	Sequence 6748, Ap
39	149	7.6	248	4	US-09-198-452A-417	Sequence 417, App
40	141.5	7.3	909	4	US-09-352-991A-30503	Sequence 30503, A
41	137	7.0	245	4	US-09-352-991A-17232	Sequence 17232, A
42	118	6.0	249	4	US-09-134-001C-4777	Sequence 4777, Ap
43	117	6.0	283	4	US-09-352-991A-22696	Sequence 22696, A
44	92	4.7	1104	4	US-09-368-347-28	Sequence 28, Appli
45	92	4.7	1104	4	US-09-368-347-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-09-973-963-4
; Sequence 4, Application US/09973963
; Patent No. 6653102
; GENERAL INFORMATION:
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul L.
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
; FILE REFERENCE: Protein Interactions in ND
; CURRENT APPLICATION NUMBER: US/09/973,963
; CURRENT FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: US 60/240,790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: US 60/304,775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-973-963-4

Query Match 100.0%; Score 1951; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 5.3e-193;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
Db 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRFPDGGSGSPAT 60
QY 61 WDNFGIWDNRIDPILLPPSIKYGKPIPKISLENVGCASQIGKRKKNEDRDFPAQLTDEV 120
Db 61 WDNFGIWDNRIDPILLPPSIKYGKPIPKISLENVGCASQIGKRKKNEDRDFPAQLTDEV 120
QY 121 LYFAVYDGHGPGAAADFCHTHMEKIMDLLPKKNLETLTLAFLEIDKAFSSHARUSAD 180
Db 121 LYFAVYDGHGPGAAADFCHTHMEKIMDLLPKKNLETLTLAFLEIDKAFSSHARUSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGPVKMLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKGPVKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVANNISLQPHVNGRLANTRISIGDLDKTSVIAEPETKRIKLHADDLSFLVLTDDGI 300
Db 241 GGFVANNISLQPHVNGRLANTRISIGDLDKTSVIAEPETKRIKLHADDLSFLVLTDDGI 300
QY 301 NFVNSQEIICDFVNOCHDPNEAAHAHVTEQAIQYGTEDNSTAVVVPFGAWGKYKNSEINFS 360

Db 301 NFVNSQEI CDVFNQCHDPNEAAHVA TEQAIOGTEDNSTAVVPTFGAWGKYKXNSEIFS 360
QY 361 FSRFSASSGRWA 372
Db 361 FSRFSASSGRWA 372

RESULT 2
US-08-822-701-9
; Sequence 9, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; US-08-822-701-9

Query Match 16.7%; Score 325; DB 2; Length 281;
Best Local Similarity 32.8%; Pred. No. 3.7e-25;
Matches 79; Conservative 48; Mismatches 82; Indels 32; Gaps 7;

QY 122 YFAYVDGHHGGAADFCHTHMEKIMD--LLPKENLETLTLTFLAFLEIDKAFSSHARLSA 179
Db 53 YFAYVDGHHGGAADFCHTHMEKIMD--LLPKENLETLTLTFLAFLEIDKAFSSHARLSA 179

QY 180 DATLLTSGTTATVALLR-----DGI-----ELVVASVGDSRAILCRKGKPKMLT 223
Db 107 -KLVNSGCTAAVCVLRWELPDSVSDSDMLAQHQRKLYTANVGDSRVLFRNGNSIRLT 165

QY 224 IDHTPERKDEKERTKCGGFVAVNSLQGFVHNGSLAMTRSGIDLDLKTSGVIAEPETKRI 283
Db 166 YDHKASDTLEVRQVEQAGGLIM-----KSRVNGMLAVTRSLGD-KFFDSLVLVGSPTTSV 219

QY 284 KLHADDSDFLVLTGDTGTFNFMVNSQEI CDVFNQCHDPNEAAHVA TEQAIOGTEDNSTAVV 343
Db 220 EI-TSEDKFLILACDGLWDVDDQACELIKDITEPNEAAKVLVRYALENGTTDNTVTVMV 278

Db 220 EI-TSEDKFLILACDGLWDVDDQACELIKDITEPNEAAKVLVRYALENGTTDNTVTVMV 278
QY 344 V 344
Db 279 V 279

RESULT 3
US-08-935-855-9
; Sequence 9, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; US-08-935-855-9

Query Match 16.7%; Score 325; DB 3; Length 281;
Best Local Similarity 32.8%; Pred. No. 3.7e-25;
Matches 79; Conservative 48; Mismatches 82; Indels 32; Gaps 7;

QY 122 YFAYVDGHHGGAADFCHTHMEKIMD--LLPKENLETLTLTFLAFLEIDKAFSSHARLSA 179
Db 53 YFAYVDGHHGGAADFCHTHMEKIMD--LLPKENLETLTLTFLAFLEIDKAFSSHARLSA 179

QY 180 DATLLTSGTTATVALLR-----DGI-----ELVVASVGDSRAILCRKGKPKMLT 223
Db 107 -KLVNSGCTAAVCVLRWELPDSVSDSDMLAQHQRKLYTANVGDSRVLFRNGNSIRLT 165

QY 224 IDHTPERKDEKERTKCGGFVAVNSLQGFVHNGSLAMTRSGIDLDLKTSGVIAEPETKRI 283
Db 166 YDHKASDTLEVRQVEQAGGLIM-----KSRVNGMLAVTRSLGD-KFFDSLVLVGSPTTSV 219

QY 284 KLHADDSDFLVLTGDTGTFNFMVNSQEI CDVFNQCHDPNEAAHVA TEQAIOGTEDNSTAVV 343
Db 220 EI-TSEDKFLILACDGLWDVDDQACELIKDITEPNEAAKVLVRYALENGTTDNTVTVMV 278

QY 344 V 344
DB 279 V 279

RESULT 4

US-08-873-093-3
; Sequence 3, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1247927
US-08-873-093-3

Query Match 16.4%; Score 319.5; DB 2; Length 390;
Best Local Similarity 31.6%; Pred. No. 2.3e-24;
Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;
QY 88 PKISLENV-----GCASQIGKXKXENEDR-----FDPAQLTDEVLYFAVYDGHGGPAA 134
DB 8 PKTEKHNAHGAGNGLRYGLSSMQGWVEMEDAHAVVGIPHGLEDWSFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EKCIMDLLPKENKLETLTLTAFLTDKAFSSHARLSADA 181
DB 68 ANYCSTHLEHTTNEEDFRAADKSGFALEPSVENVTGIRGTGLKIDYMRNFSDLRNG- 126
QY 182 TLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKPKMKLTIDHTPERKDEKRIKKG 241
DB 127 -MDRSGSTA-VGMWISPTHIYFINGDSRAVLCRNGQVCFSTQDHKPCNPKMEKRIQAG 184
QY 242 GFVAMNSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHADDSDL 293
DB 185 G-----SVMIQRVNGSLAVSRALGDYDKVCDGKGPTEQLVSPPEVYEI-LRAEEDFV 238

QY 294 VLTDDGINFMVNSQEICDFVNO-----CHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPF 346
DB 239 VLACDGIWDMVNSNEELCEFVNSRLSVLESDDLNVCNWWVDTCLHKGRDRNMSIVLVCF 295

RESULT 5

US-09-206-646-3
; Sequence 3, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; FILE REFERENCE: PF-0319-1 DIV
; CURRENT APPLICATION NUMBER: US/09/206,646
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: ID No. 6436637 9247927
US-09-206-646-3

Query Match 16.4%; Score 319.5; DB 4; Length 390;
Best Local Similarity 31.6%; Pred. No. 2.3e-24;
Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;
QY 88 PKISLENV-----GCASQIGKXKXENEDR-----FDPAQLTDEVLYFAVYDGHGGPAA 134
DB 8 PKTEKHNAHGAGNGLRYGLSSMQGWVEMEDAHAVVGIPHGLEDWSFFAVYDGHAGSRV 67
QY 135 ADFCHTHM-----EKCIMDLLPKENKLETLTLTAFLTDKAFSSHARLSADA 181
DB 68 ANYCSTHLEHTTNEEDFRAADKSGFALEPSVENVTGIRGTGLKIDYMRNFSDLRNG- 126
QY 182 TLLTSGTTATVALLRDGIELVVASVGDSSRAILCRKPKMKLTIDHTPERKDEKRIKKG 241
DB 127 -MDRSGSTA-VGMWISPTHIYFINGDSRAVLCRNGQVCFSTQDHKPCNPKMEKRIQAG 184
QY 242 GFVAMNSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHADDSDL 293
DB 185 G-----SVMIQRVNGSLAVSRALGDYDKVCDGKGPTEQLVSPPEVYEI-LRAEEDFV 238
QY 294 VLTDDGINFMVNSQEICDFVNO-----CHDPNEAAHAHVTEQAIOYGTEDNSTAVVVPF 346
DB 239 VLACDGIWDMVNSNEELCEFVNSRLSVLESDDLNVCNWWVDTCLHKGRDRNMSIVLVCF 295

RESULT 6

US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto


```

; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 195647
; US-09-013-881-2

Query Match 16.1%; Score 314; DB 3; Length 392;
Best Local Similarity 27.5%; Pred. No. 8.6e-24;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LLODDRVTPTCHSSTSEPCRSRFPDGGSPATWDFGIWDRIDEPILLPPSI----- 81
Db 27 LLFDD---LPPASSTDS-----GSGPLLFDD-----LPPASGGDSG 60

QY 82 -----KYPKISLENVGCASQIGKRK-ENED 109
Db 61 SLATSIQVMKTEGKAKRTSSEKNGSEELVEKKVKCRASSVIFGLKGVVAERKGEREE 120

QY 110 RFD-----FAQLTDE-----VLYFAYDGGHGGPAAADFCHTHMEKIMDLLPK--- 152
Db 121 MQDAHVLINDITECRPPSSSLITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180

QY 153 ---EKNLETLTLTFLAFLIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVAVSGDS 209
Db 181 ISVEKTVKRCLLDTFKHTDBEFLLKQA--SSQKPAWKDGGSTATCVLAVDNI-LYIANLGDS 237

QY 210 RAILCR-----KGGPKMLTIDHTPERKOEKERIKKCGGFVAMNSLGQPHVNGRLAMTRS 263
Db 238 RAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAGG-----NVRDGRVLGVLEVSRS 292

QY 264 IGDLDLKTSGVIAPEPKRIKLHADDLSFLVLTDDGINFMWNSOEICDFVNOCHDNE-- 321
Db 293 IGDQYKRCGVTSVPDIRRCQL--TPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351

QY 322 -----AAHAVTEQAIQYGTEDNSTAVVVPFG 347
Db 352 TREKSAADARYEAACNRLANKAVQGSADNVTVWVRIG 391

RESULT 7
US-09-612-473-2
; Sequence 2, Application US/09612473
; Patent No. 6518029
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga

```

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; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Gugler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; FILE REFERENCE: PF-0470-1 CIP
; CURRENT APPLICATION NUMBER: US/09/612,473
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/013,881
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6518029 195647
; US-09-612-473-2

Query Match 16.1%; Score 314; DB 4; Length 392;
Best Local Similarity 27.5%; Pred. No. 8.6e-24;
Matches 110; Conservative 56; Mismatches 120; Indels 114; Gaps 15;

QY 27 LLODDRVTPTCHSSTSEPCRSRFPDGGSPATWDFGIWDRIDEPILLPPSI----- 81
Db 27 LLFDD---LPPASSTDS-----GSGPLLFDD-----LPPASGGDSG 60

QY 82 -----KYPKISLENVGCASQIGKRK-ENED 109
Db 61 SLATSIQVMKTEGKAKRTSSEKNGSEELVEKKVKCRASSVIFGLKGVVAERKGEREE 120

QY 110 RFD-----FAQLTDE-----VLYFAYDGGHGGPAAADFCHTHMEKIMDLLPK--- 152
Db 121 MQDAHVLINDITECRPPSSSLITRVSYFAVFDGHHGIRASKFAAQNHLQNLIRKPKGDV 180

QY 153 ---EKNLETLTLTFLAFLIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVAVSGDS 209
Db 181 ISVEKTVKRCLLDTFKHTDBEFLLKQA--SSQKPAWKDGGSTATCVLAVDNI-LYIANLGDS 237

QY 210 RAILCR-----KGGPKMLTIDHTPERKOEKERIKKCGGFVAMNSLGQPHVNGRLAMTRS 263
Db 238 RAILCRYNESQKHAALSLSKEHNPTQYERMRIOKAGG-----NVRDGRVLGVLEVSRS 292

QY 264 IGDLDLKTSGVIAPEPKRIKLHADDLSFLVLTDDGINFMWNSOEICDFVNOCHDNE-- 321
Db 293 IGDQYKRCGVTSVPDIRRCQL--TPNDRFILLACDGLFKVFTPEEAVNFILSCLEDEKIQ 351

QY 322 -----AAHAVTEQAIQYGTEDNSTAVVVPFG 347
Db 352 TREKSAADARYEAACNRLANKAVQGSADNVTVWVRIG 391

RESULT 8
US-09-206-646-4
; Sequence 4, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti G.
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; FILE REFERENCE: PF-0319-1 DIV
; CURRENT APPLICATION NUMBER: US/09/206,646
; CURRENT FILING DATE: 2001-12-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 390

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; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
US-08-935-855-8

Query Match 15.7%; Score 306.5; DB 3; Length 306;
Best Local Similarity 31.0%; Pred. No. 3.5e-23;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

QY 88 PKISLENY-----GCASQIGKRENEDEDR-----FDFAQLTDEVLYFAVYDGHGGPAA 134
DB 8 PKMEKHNAQGGNGRLRYGLSSQGWVRVEMEDAHAVVGVIPHGLDNWAFVYDGHAGSRV 67
QY 135 ADPCHTMEKIMDL-----LPKEKNLETLTLAFLAIDK--AFSSSHARLSADATLL 184
DB 68 AKYCEHLLDHTNNQDFKGSAGAPSVENVKNGIRGTGFLAIDEMRVMSKKHGAD---- 123
QY 185 TSGTTATVALLRDGIELVAVSGDSRAILCRKKGPKMLTIDHTPERKDEKERIKKCGFV 244
DB 124 RSGSTA-VGVLISSPQHTYFVINGDSRGLLGRNRKRVHFFTDHKPSPLEKRIQNAAG-- 180
QY 245 AWWNSLQPHVNGRLAMTRISIGDLK-----TSGVIA--EPETKRIKLHADDSEFLVLT 296
DB 181 ---SVMIQKRVNGSLAVSRALGDYFKVHGKGPTEQLVSPPEVPEVHDIERSEEDDQFIILA 237
QY 297 TDGINFMVNSQIEICDFVQ-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
DB 238 CDGIWDVNGNEELCDFVRSRLVETDDEKVCNEVVDTCLYKGRDNMSVILICF 291

RESULT 11
US-08-822-701-7
; Sequence 7, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:

; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-822-701-7

Query Match 15.4%; Score 300; DB 2; Length 309;
Best Local Similarity 31.3%; Pred. No. 1.7e-22;
Matches 93; Conservative 47; Mismatches 109; Indels 48; Gaps 11;

QY 88 PKISLENY-----GCASQIGKRENEDEDR-----FDFAQLTDEVLYFAVYDGHGGPAA 134
DB 8 PKTEKHNAHAGNGRLRYGLSSQGWVRVEMEDAHAVVGVIPHGLDNWAFVYDGHAGSRV 67
QY 135 ADPCHTMEKIMDL-----EKIMDLPLKEKNLETLTLAFLAIDKAFSSSHARLSADA 181
DB 68 ANYCSTHLEHITTTNEDFRAADKSGSALESPVESVKTGRT-GFLKIDFYMRNFDLRLNG- 125
QY 182 TLLTSGTTATVALLRDGIELVAVSGDSRAILCRKKGPKMLTIDHTPERKDEKERIKKCG 241
DB 126 -MDRSGSTA-VGVWVSPHTMYFVINGDSRAVLCRNGQVCFSTQDKPCNPVEKERIQNAG 183
QY 242 GFVANNLSQPHVNGRLAMTRISIGDLK-----TSGVIA--BPETKRIKLHADDSEFL 293
DB 184 G-----SVMIQKRVNGSLAVSRALGDYFKVHGKGPTEQLVSPPEVPEVYI--VRAEEDFV 237
QY 294 VLTDTGINFMVNSQIEICDFVQ-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
DB 238 VLACDGIWDVMSNEELCFVRSRLVSDLENCVNVVVDTCCHKGSRDNMSVILVCF 294

RESULT 12
US-08-935-855-7
; Sequence 7, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:

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; ORGANISM: Mus musculus
US-08-935-855-7

Query Match      15.4%; Score 300; DB 3; Length 309;
Best Local Similarity 31.3%; Pred. No. 1.7e-22;
Matches 93; Conservative 47; Mismatches 109; Indels 48; Gaps 11;

QY 88 PKISLENV-----GCASQIGKRKENEDR-----FDFQAQTDEVLVFAVYDGHGGPAA 134
Db 8 PKTEKNAHAGNGLRYGLSSMQGWRVEMEDAHAVVGIPIHGLDWNWSPFAVYDGHAGSRV 67

QY 135 ADFCHTHM-----EKCIMDLPLKKNLETLTLAFLEIDKAFSSHARLSADA 181
Db 68 ANYCSTHLEHTTNEEDFPAAGKSGSALELSVENVKNIGRTGFLKIDEMRNFSDLRNG- 125

QY 182 TLLTSGTTATVALLRDGIELVVASVGDRAILCRKGPKMKLTIDHTPERKDEKERIKCG 241
Db 126 -MDRSGSTA-VGVMISPKHIVFINGDSRAVLRYNGQVCFSTQDHKPCNPVEKERIQAG 183

QY 242 GFVAVNSLQPHVNGELAMTRISIGDLDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
Db 184 G-----SVMTQRVNGSLAVSRALGDYDKCVGKGPTQOLVSPPEVYEI-VRAEEDBFV 237

QY 294 VLTTDGINFMVNSQEICDFVNC-----CHDPNEAAHAAVTEQAIQYGTEDNSTAVVVPF 346
Db 238 VLACDGIWDVMSNEELCEPVKSRLEVSDDLENVCNVWVDTCLHKGRDNMSIVLVCF 294

RESULT 13
US-08-873-093-1
; Sequence 1, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIPLB01
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; CLONE: 13177
US-08-873-093-1

Query Match      14.5%; Score 282.5; DB 2; Length 478;
Best Local Similarity 29.2%; Pred. No. 2.1e-20;
Matches 92; Conservative 53; Mismatches 117; Indels 53; Gaps 11;

QY 88 PKISLENV-----GCASQIGKRKENEDR-----FDFQAQTDEVLVFAVYDGHGGPAA 134
Db 8 PKTEKNAHAGNGLRYGLSSMQGWRVEMEDAHAVVGIPIHGLDWNWSPFAVYDGHAGSRV 67

QY 135 ADFCHTHM-----EKCIMDLPLKKNLETLTLAFLEIDKAFSSHARLSADA 181
Db 68 ANYCSTHLEHTTNEEDFPAAGKSGSALELSVENVKNIGRTGFLKIDEMRNFSDLRNG- 126

QY 182 TLLTSGTTATVALLRDGIELVVASVGDRAILCRKGPKMKLTIDHTPERKDEKERIKCG 241
Db 127 -MDRSGSTA-VGVMISPKHIVFINGDSRAVLRYNGQVCFSTQDHKPCNPVEKERIQAG 184

QY 242 GFVAVNSLQPHVNGELAMTRISIGDLDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
Db 185 G-----SVMTQRVNGSLAVSRALGDYDKCVGKGPTQOLVSPPEVYEI-LRAEEDFI 238

QY 294 VLTTDGINFMVNSQEICDFVNC-----CHDPNEAAHAAVTEQAIQYGTEDNSTAVVVPF 349
Db 239 ILACDGIWDVMSNEELCEPVKSRLEVSDDLENVCNVWVDTCLHKGRDNMSIVLVCF 298

QY 350 GK-----KNSEIN 358
Db 299 PKVSDAVKKDSELD 313

RESULT 14
US-08-873-093-4
; Sequence 4, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
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STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 1452526
 US-08-873-093-4

Query Match 14.5%; Score 282.5; DB 2; Length 478;

Best Local Similarity 29.2%; Pred. No. 2.1e-20;
 Matches 92; Conservative 53; Mismatches 117; Indels 53; Gaps 11;

QY 88 PKISLENY-----GCASQIGKRKENEDR-----FDFALQTDDEVLYFAYVDGHGCPAA 134
 DB 8 PKTEKHNAHGAGNGLRYGLSSMQGWRVEMEDAHAVVGI PHGLEDSFFFAVDGHAGSRV 67
 QY 135 ADFCHTMEKICMD-----LLPKKLETLTLTFLAFLEIDKAFSSSHARLSADA 181
 DB 68 ANYCSTHLEHITTNEEDFRAAGKSGSALELSVENVKNGIRTGFLKIDEXNRNFSDLRNG- 126
 QY 182 TLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKCG 241
 DB 127 -MDRSGSTA-VGVWISPKHIYFINGDSRAVLRYNGQVCFSTQDHKPCNPREKERIQNAG 184
 QY 242 GFVAVNSLQOPHYNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
 DB 185 G-----SVMIQRVNGSLAVSRALGDYKCVGKGTEQLVSPPEVYEI-LRAEDEFI 238
 QY 294 VLTGGINFMVNSOEICDFVNO-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPFGAW 349
 DB 239 ILACDGIWVNSNEELCEYVKSRLEVSDDLENVCNVVDTCLHKGSRDNMSIVLVCFNSA 298
 QY 350 GKY-----KNSEIN 358
 DB 299 PKVSDEAVKDSELD 313

RESULT 15

US-09-206-646-1

; Sequence 1, Application US/09206646

; Patent No. 6436637

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Goli, Surya K.

; APPLICANT: Lal, Preeti G.

; APPLICANT: Corley, Neil C.

; APPLICANT: Zhang, Hong

; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE

; FILE REFERENCE: PF-0319-1 DIV

; CURRENT APPLICATION NUMBER: US/09/206,646

; CURRENT FILING DATE: 2001-12-07

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PERL Program

; SEQ ID NO 1

; LENGTH: 479

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURES:

; NAME/KEY: misc.feature

; OTHER INFORMATION: Incyte ID No. 6436637 013177CDI

US-09-206-646-1

Query Match

14.5%; Score 282.5; DB 4; Length 479;

Best Local Similarity 29.2%; Pred. No. 2.1e-20;
 Matches 92; Conservative 53; Mismatches 117; Indels 53; Gaps 11;

QY 88 PKISLENY-----GCASQIGKRKENEDR-----FDFALQTDDEVLYFAYVDGHGCPAA 134
 DB 8 PKTEKHNAHGAGNGLRYGLSSMQGWRVEMEDAHAVVGI PHGLEDSFFFAVDGHAGSRV 67
 QY 135 ADFCHTMEKICMD-----LLPKKLETLTLTFLAFLEIDKAFSSSHARLSADA 181
 DB 68 ANYCSTHLEHITTNEEDFRAAGKSGSALELSVENVKNGIRTGFLKIDEXNRNFSDLRNG- 126

QY 182 TLLTSGTTATVALLRDGIELVAVSGDSRAILCRKPKMKLTIDHTPERKDEKERIKKCG 241
 DB 127 -MDRSGSTA-VGVWISPKHIYFINGDSRAVLRYNGQVCFSTQDHKPCNPREKERIQNAG 184
 QY 242 GFVAVNSLQOPHYNGRLAMTRISIGDLK-----TSGVIA-EPETKRIKLHHADDSFL 293
 DB 185 G-----SVMIQRVNGSLAVSRALGDYKCVGKGTEQLVSPPEVYEI-LRAEDEFI 238
 QY 294 VLTGGINFMVNSOEICDFVNO-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPFGAW 349
 DB 239 ILACDGIWVNSNEELCEYVKSRLEVSDDLENVCNVVDTCLHKGSRDNMSIVLVCFNSA 298
 QY 350 GKY-----KNSEIN 358
 DB 299 PKVSDEAVKDSELD 313

Search completed: October 12, 2004, 06:00:46
 Job time : 108 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 98 Seconds
(without alignments)
1197.681 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSQGNQVRRR.....KNSINFSSRSFSSGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1951	100.0	372	4 Q8N3J5	Q8N3J5 homo sapien
2	1930	99.9	372	4 Q96NT4	Q96NT4 homo sapien
3	1945	99.7	372	4 Q8IUT7	Q8IUT7 homo sapien
4	1777	91.1	372	11 Q8BXN7	Q8BXN7 mus musculus
5	951.5	48.8	233	4 Q8IXG7	Q8IXG7 homo sapien
6	950	48.7	182	4 Q8ND70	Q8ND70 homo sapien
7	369	18.9	354	10 Q8LAY8	Q8LAY8 arabidopsis
8	360	18.5	348	10 Q8LEW5	Q8LEW5 arabidopsis
9	357	18.3	383	10 Q8WIP8	Q8WIP8 arabidopsis
10	352	18.0	282	10 Q7XR05	Q7XR05 oryza sativ
11	350.5	18.0	303	11 Q810H0	Q810H0 mus musculus
12	350.5	18.0	360	11 Q8C021	Q8C021 mus musculus
13	350.5	18.0	360	11 Q8BHN0	Q8BHN0 mus musculus
14	348	17.8	319	10 Q8S8Z0	Q8S8Z0 mesembryant
15	346.5	17.8	368	10 Q8H610	Q8H610 oryza sativ
16	344.5	17.7	392	10 Q9SLAI	Q9SLAI arabidopsis

17	344	17.6	311	10 Q8RXV3	Q8RXV3 arabidopsis
18	344	17.6	420	10 Q8VZD9	Q8VZD9 arabidopsis
19	342	17.5	394	10 Q84QD6	Q84QD6 nicotiana t
20	342	17.5	420	10 Q94AT1	Q94AT1 arabidopsis
21	340.5	17.5	380	10 Q9FYN7	Q9FYN7 oryza sativ
22	337.5	17.3	381	10 Q24078	Q24078 medicago sa
23	335	17.2	243	10 Q8G3P1	Q8G3P1 oryza sativ
24	334.5	17.1	362	10 Q92PL9	Q92PL9 lotus japon
25	334.5	17.1	380	10 Q8S8Z1	Q8S8Z1 mesembryant
26	333.5	17.1	371	10 Q8VZN9	Q8VZN9 arabidopsis
27	332.5	17.0	359	10 Q82469	Q82469 mesembryant
28	332	17.0	283	10 Q81714	Q81714 arabidopsis
29	332	17.0	467	10 Q81J68	Q81J68 oryza sativ
30	328	16.8	362	10 Q9ZW21	Q9ZW21 arabidopsis
31	326	16.7	307	10 Q9FCM3	Q9FCM3 arabidopsis
32	326	16.7	464	10 Q9FXE4	Q9FXE4 arabidopsis
33	324.5	16.6	511	10 Q8GWS8	Q8GWS8 arabidopsis
34	322.5	16.5	239	10 Q64S83	Q64S83 arabidopsis
35	322.5	16.5	528	10 Q93YS2	Q93YS2 arabidopsis
36	322.5	16.5	816	10 Q9M1V6	Q9M1V6 arabidopsis
37	322	16.5	283	10 Q94AE3	Q94AE3 arabidopsis
38	322	16.5	396	10 Q9LP12	Q9LP12 arabidopsis
39	322	16.5	511	10 Q9CAJ0	Q9CAJ0 arabidopsis
40	322	16.5	511	10 Q81709	Q81709 arabidopsis
41	321	16.5	271	10 Q9SM39	Q9SM39 sporobolus
42	320	16.4	355	10 Q81716	Q81716 arabidopsis
43	319.5	16.4	317	10 Q7XPM4	Q7XPM4 oryza sativ
44	319.5	16.4	389	10 Q81773	Q81773 arabidopsis
45	319.5	16.4	465	11 Q99ND8	Q99ND8 ratrus norv

ALIGNMENTS

RESULT 1

Q8N3J5 PRELIMINARY; PRT; 372 AA.

AC Q8N3J5; Q8N3J5; (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

GN DKFZP761G058.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Amgdala;

RA Koshner K., Beyer A., Mewes H.W., Weil B., Wiemann S.;

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL834271; CAD38946.1; -

DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.

DR GO; GO:0003824; F:catalytic activity; IEA.

DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.

DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.

DR InterPro; IPR000222; PP2C.

DR InterPro; IPR001932; PP2C-like.

DR Pfam; PF00481; PP2C; 1.

DR SMART; SM00332; PP2C; 1.

DR SMART; SM00331; PP2C SIG; 1.

DR PROSITE; PS01032; PP2C; 1.

KW Hypothetical protein.

SQ SEQUENCE 372 AA; 49997 MW; 9DD37EECOEAD3313 CRC64;

Query Match 100.0%; Score 1951; DB 4; Length 372;

Best Local Similarity 100.0%; Pred. No. 7.5e-160;

Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDPDGSQSPAT 60
|||||

Db 1 MSTAALITLVRSQGNQVRRVLLSSRLLODDRVTPTCHSSTSEPRCSRDPDGSQSPAT 60
|||||

QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
 QY 121 LYFAYVDGHHGGAADFCHTHMEKICIMDLLPKENKLETLTLAFLAIDKAFSSHARLSAD 180
 Db 121 LYFAYVDGHHGGAADFCHTHMEKICIMDLLPKENKLETLTLAFLAIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLGOPHNGRLAMTRISIGDLTKTSGVIABPETKRIKLHADDSEFLVLTDDGI 300
 Db 241 GGFVAMNSLGOPHNGRLAMTRISIGDLTKTSGVIABPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 Db 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 QY 361 FSRSFASSGRWA 372
 Db 361 FSRSFASSGRWA 372

RESULT 2

Q96NT4 ID Q96NT4 PRELIMINARY; PRT; 372 AA.
 AC Q96NT4; 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ30116.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Cerebellum;
 RA Nishi T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M.,
 RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
 RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
 RA Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
 RT "NEDO human cDNA sequencing project."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 DR EMBL; AK054678; BAB70790.1; -;
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0000287; F:magnesium ion binding; IEA.
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C SIG; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein; Hydrolase; Magnesium.
 SQ SEQUENCE 372 AA; 40963 MW; 7065B29DC79C93B CRC64;

Query Match 99.9%; Score 1950; DB 4; Length 372;
 Best Local Similarity 99.7%; Pred. No. 9.2e-160;
 Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGGNQVRRVLLSSRLLODDRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSGGNQVRRVLLSSRLLODDRVTPTCHSSTSPRCRFPDGGSGSPAT 60

QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
 QY 121 LYFAYVDGHHGGAADFCHTHMEKICIMDLLPKENKLETLTLAFLAIDKAFSSHARLSAD 180
 Db 121 LYFAYVDGHHGGAADFCHTHMEKICIMDLLPKENKLETLTLAFLAIDKAFSSHARLSAD 180
 QY 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 Db 181 ATLLTSGTTATVALLRGGIELVWASVGDRAILCRKGKPKMLTIDHTPERKDEKERIKKC 240
 QY 241 GGFVAMNSLGOPHNGRLAMTRISIGDLTKTSGVIABPETKRIKLHADDSEFLVLTDDGI 300
 Db 241 GGFVAMNSLGOPHNGRLAMTRISIGDLTKTSGVIABPETKRIKLHADDSEFLVLTDDGI 300
 QY 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 Db 301 NFMVNSQICDFVNOCHDPNEAAHVAITEQAIOYGTEDNSTAVVVPFGAWGKYKXSEINFS 360
 QY 361 FSRSFASSGRWA 372
 Db 361 FSRSFASSGRWA 372

RESULT 3

Q8IUZ7 ID Q8IUZ7 PRELIMINARY; PRT; 372 AA.
 AC Q8IUZ7; 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pancreas;
 RA Strausberg R.;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC037552; AAH37552.1; -;
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR SMART; SM00331; PP2C SIG; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 372 AA; 41011 MW; 29927CBB2EDD32A2 CRC64;

Query Match 99.7%; Score 1945; DB 4; Length 372;
 Best Local Similarity 99.7%; Pred. No. 2.5e-159;
 Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSGGNQVRRVLLSSRLLODDRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 Db 1 MSTAALITLVRSGGNQVRRVLLSSRLLODDRVTPTCHSSTSPRCRFPDGGSGSPAT 60
 QY 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
 Db 61 WDNFGIWNDRIDEPIILLPPSIKYGKPIPKISLENVGCASQIGKRNEDRDFPAQLTDEV 120
 QY 121 LYFAYVDGHHGGAADFCHTHMEKICIMDLLPKENKLETLTLAFLAIDKAFSSHARLSAD 180
 Db 121 LYFAYVDGHHGGAADFCHTHMEKICIMDLLPKENKLETLTLAFLAIDKAFSSHARLSAD 180

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QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSPRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
Db 181 ATLLTSGTTATVALLRDGIELVVASVGDSPRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVAVNSLIGQPHVNGRLANTRISIGDLDLKTSQVIAEPETTKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLIGQPHVNGRLANTRISIGDLDLKTSQVIAEPETTKRIKLHHADDSFLVLTDDGI 300
QY 301 NFWVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINFNS 360
Db 301 NFWVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINFNS 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 4
Q8BXN7 PRELIMINARY; PRT; 372 AA.
AC Q8BXN7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein serine/threonine phosphatase 2C structure
DE containing protein.
GN A930026L03RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Retina;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL 60,770 full-length cDNAs.";
DR EMBL; AK044610; BAC32001.1; -.
DR PIR; PT0546; PT0698.
DR MGI; MGI:2442111; A930026L03RIK.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR001932; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2CC; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hypothetical protein.
SQ SEQUENCE 372 AA; 40918 MW; 3749BB94F211E7A CRC64;

Query Match 91.1%; Score 1777; DB 11; Length 372;
Best Local Similarity 90.3%; Pred. No. 7.8e-145;
Matches 336; Conservative 18; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSTSEPRCSRFPDPGSGSPAT 60
Db 1 MLSAAITLVRSNGQVRRVLLSSRLLODDRVTPTCHSTSEPRCSRFPDPGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKREKEDRFPDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASLIGKREKEDRFPDFAQLTDEV 120
QY 121 LYFAVVDGHHGPPAAADFCHTHMEKCIWDLLEPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVVDGHHGPPAAADFCHTHMEKCIWDLLEPKENLETLTLTFLAFLEIDKAFASYARLSAD 180
QY 181 ATLLTSGTTATVALLRDGIELVVASVGDSPRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
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Db 181 ASLLTSGTTATVALLRDGIELVVASVGDSPRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
QY 241 GGFVAVNSLIGQPHVNGRLANTRISIGDLDLKTSQVIAEPETTKRIKLHHADDSFLVLTDDGI 300
Db 241 GGFVAVNSLIGQPHVNGRLANTRISIGDLDLKTSQVIAEPETTKRIKLHHADDSFLVLTDDGI 300
QY 301 NFWVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINFNS 360
Db 301 NFWVNSQICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVVVPFGAWGKYKNSINFNS 360
QY 361 FSRSPASSGRWA 372
Db 361 FSRSPASSGRWA 372

RESULT 5
Q8IXG7 PRELIMINARY; PRT; 233 AA.
AC Q8IXG7;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE UG0882E07.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RX "Isolation of full-length cDNA clones from human fetal brain cDNA
library.";
RL EMBL; AF351614; AAN76514.1; -.
DR PIR; PT0240.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR001932; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 233 AA; 25692 MW; EB90A7B3BC1BDD08 CRC64;

Query Match 48.8%; Score 951.5; DB 4; Length 233;
Best Local Similarity 86.6%; Pred. No. 6.9e-74;
Matches 187; Conservative 5; Mismatches 17; Indels 7; Gaps 1;

QY 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSTSEPRCSRFPDPGSGSPAT 60
Db 1 MSTAALITLVRSNGQVRRVLLSSRLLODDRVTPTCHSTSEPRCSRFPDPGSGSPAT 60
QY 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKREKEDRFPDFAQLTDEV 120
Db 61 WDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENVGCASQIGKREKEDRFPDFAQLTDEV 120
QY 121 LYFAVVDGHHGPPAAADFCHTHMEKCIWDLLEPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180
Db 121 LYFAVVDGHHGPPAAADFCHTHMEKCIWDLLEPKENLETLTLTFLAFLEIDKAFSSHARLSAD 180
QY 181 ATLLTSGT-----TATVALLRDGIELVVASVGDSPRAILCRKKGPKMLTIDHTPERKDEKERIKK 240
Db 181 ENCWSAALDLEFVDVDTTCGASVEREICILLSQVKES 216

RESULT 6
Q8ND70 PRELIMINARY; PRT; 182 AA.
AC Q8ND70;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
```


DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN DKFZP667B084.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymph node.
 RA Ansoerger W., Wirtner U., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL834167; CAD38869.1; -
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 182 AA; 20239 MW; 0D2523DB99A810BB CRC64;

 Query Match 48.7%; Score 950; DB 4; Length 182;
 Best Local Similarity 100.0%; Pred. No. 6.5e-74;
 Matches 180; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 MSTAALITLVRSGNQVRRVLLSSRLQLQDRVTPCHSSTSEPRCSRDPDGGSGSPAT 60
 DB 1 MSTAALITLVRSGNQVRRVLLSSRLQLQDRVTPCHSSTSEPRCSRDPDGGSGSPAT 60

 QY 61 WDNFGIWNDRIDEPIILPPSIKYGKPTPKISLENVGCASQIGRKENEDRFPDPAQLTDEV 120
 DB 61 WDNFGIWNDRIDEPIILPPSIKYGKPTPKISLENVGCASQIGRKENEDRFPDPAQLTDEV 120

 QY 121 LYFAVYDGHGGPAAADFCHTHMEKINDLLPKENKLTTLTFLAFLEIDKAFSSHARLSAD 180
 DB 121 LYFAVYDGHGGPAAADFCHTHMEKINDLLPKENKLTTLTFLAFLEIDKAFSSHARLSAD 180

 RESULT 7
 Q8LAY8 PRELIMINARY; PRT; 354 AA.
 AC Q8LAY8;
 ID Q8LAY8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DE Protein phosphatase 2C-like protein (Hypothetical protein).
 GN AT5G10740/T3ON20 10 OR AT5G10740.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 ON NCBI_TaxID=3702;
 [1]
 RP SEQUENCE FROM N.A.
 RA Haas B.J., Volkovskiy N., Town C.D., Troukhan M., Alexandrov N.,
 RA Feldmann K.A., Flavell R.B., White O., Salzberg S.L.;
 RT "Full-length messenger RNA sequences greatly improve genome
 RT annotation.";
 RL Genome Biol. 0:0-0(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,

RA Hayashizaki Y., Shinozaki K.;
 RT "Arabidopsis thaliana full-length cDNA";
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE FROM N.A.
 RP Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
 RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
 RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
 RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
 RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
 RA Schwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
 RA Theologis A.;
 RT "Arabidopsis Open Reading Frame (ORF) Clones";
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY087522; AAM65064.1; -
 DR EMBL; AK117549; BAC4210.1; -
 DR EMBL; BT005431; AAO63851.1; -
 DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
 DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
 DR GO; GO:0005488; F:binding; IEA.
 DR GO; GO:0003824; F:catalytic activity; IEA.
 DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001933; Mitoch_carrier.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C-like.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS00331; PP2C_SIG; 1.
 DR PROSITE; PS00215; MITOCH_CARRIER; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 354 AA; 38036 MW; 87DA535B561C9D68 CRC64;

 Query Match 18.9%; Score 369; DB 10; Length 354;
 Best Local Similarity 36.1%; Pred. No. 2.3e-23;
 Matches 101; Conservative 56; Mismatches 93; Indels 30; Gaps 11;

 QY 96 GCASQIGRKENEDRFPD--FAQLTDEVL-YFAVYDGHGGPAAADFCHTHMEKINDLLPK 152
 DB 35 GYASSAGKRSMEDFFETRIDGINGEIVGLFGVDFGHGGARAAEYVVRHL---FSNLITH 91

 QY 153 EK---NLETTLLTFLAFLEID---KAFSSHARLSADATLLTSGTTATVALLRDGIELVVAS 205
 DB 92 PKFISDTKSAITDAYNHTDSELLKSENHR-----DAGSTASTAIL-VGDLRVAN 142

 QY 206 VGDRAILCRKGKPMKLTIDHTPERKOEKERIKKCGGFVAVNSLGGQPHVNGRLAMTRSIG 265
 DB 143 VGDRAVISGGKAIASVSRDKPKQSDERERENAGGFVVM--AGTWRVGGVLAVSRAFG 200

 QY 266 DLDLTKTSVIAEPETKRIKLHADD--FLVLTDTGTFNFMVNSOEICDFVNOCHDRNEAA 323
 DB 201 DRLUK-QVVAADPEIQEKI---DITLFLILASGLWDVFSNEAIVAMVKEVDEPDSA 256

 QY 324 HAVTEQAIQYCTEDNSTAVVFPFGANGKYNKSEINFPSR 363
 DB 257 KKLVGELKRGSAADNTTCVVVRFLKKSAGSSSHSSSSSK 296

 RESULT 8
 Q9LEW5 PRELIMINARY; PRT; 348 AA.
 ID Q9LEW5;
 AC Q9LEW5;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Protein phosphatase 2C-like protein.
 GN T3ON20_10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.


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Db 92 NVAVYSIQGRDHMEDRFEVLTLANKTHPSI-FGIPDHGGGTAAEYVKSRLPEALKQH 150
Qy 150 L-----PKEKNL---ETLLTLAFLDKAFSSHARLSADATLLTSGTTATVALLRDGIEL 201
Db 151 LDYKDKXNSVLTQTILEQOILSIDREMLEKLTVSVD----EAGTCLIALLSDK-DL 205
Qy 202 VVASVGDRAILCRK-GKPMKLTIDHTPERKDEKRIKCGGFVAVNSLGGQPHVNGRLAM 260
Db 206 TVANVGDGRVLCXGDNALPSLHDKPYQLKERRIKRAGGFI-SFN--GSRVVOGILAM 263
Qy 261 TRSIGDLDLKT-SGVIAEPETKRIKLHHADDSFLVLTGGINFMVNSQEIICDFVNO-CHD 318
Db 264 SRSLGDYPLKUNVWIPDPDILTFDLKQPEFMILASDGLWDAFNSAEAVRFIKERLDE 323
Qy 319 PNEAAHAHTEQAIQYGTEDNSTAVVVPFGAMGKYKNS 355
Db 324 PHFGAKSIVLQSFYSGPCPDNITVMVV-----KFRNS 354

RESULT 13
Q8BHN0 PRELIMINARY; PRT; 360 AA.
AC Q8BHN0;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CDNA FLJ30353 FIS.
GN AI481720.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Brain, and Cerebellum;
RA MEDLINE=22354683; PubMed=12466851;
RX The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573 (2002).
DR EMBL; AK035912; BAC29241.1; -.
DR EMBL; AK045724; BAC32472.1; -.
DR MGD; MGI:2139740; AI481720.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 360 AA; 41049 MW; 026AC7687E5EA1E CRC64;

Query Match 18.0%; Score 350.5; DB 11; Length 360;
Best Local Similarity 34.3%; Pred. No. 9.5e-22;
Matches 95; Conservative 52; Mismatches 101; Indels 29; Gaps 11;

Qy 94 NVGCSAQICKRKENEDRF----DFALQLTDEVLYFVYDGHGGPAAADYCHTHMEKIMDL 149
Db 92 NVAVYSIQGRDHMEDRFEVLTLANKTHPSI-FGIPDHGGGTAAEYVKSRLPEALKQH 150
Qy 150 L-----PKEKNL---ETLLTLAFLDKAFSSHARLSADATLLTSGTTATVALLRDGIEL 201
Db 151 LDYKDKXNSVLTQTILEQOILSIDREMLEKLTVSVD----EAGTCLIALLSDK-DL 205
Qy 202 VVASVGDRAILCRK-GKPMKLTIDHTPERKDEKRIKCGGFVAVNSLGGQPHVNGRLAM 260
Db 206 TVANVGDGRVLCXGDNALPSLHDKPYQLKERRIKRAGGFI-SFN--GSRVVOGILAM 263
Qy 261 TRSIGDLDLKT-SGVIAEPETKRIKLHHADDSFLVLTGGINFMVNSQEIICDFVNO-CHD 318
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Db 264 SRSLGDYPLKUNVWIPDPDILTFDLKQPEFMILASDGLWDAFNSAEAVRFIKERLDE 323
Qy 319 PNEAAHAHTEQAIQYGTEDNSTAVVVPFGAMGKYKNS 355
Db 324 PHFGAKSIVLQSFYSGPCPDNITVMVV-----KFRNS 354

RESULT 14
Q8S8Z0 PRELIMINARY; PRT; 319 AA.
AC Q8S8Z0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein phosphatase 2C.
GN MPC9.
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Aizoaceae; Mesembryanthemum.
OX NCBI_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RA Miyazaki S., Izumi S., Fukuhara T., Bohnert H.J.;
RT "Plant Protein Phosphatases 2C ? A large protein family serving
RT complex functions.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
DR EMBL; AB083482; BAB8944.1; -.
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0000287; F:magnesium ion binding; IEA.
DR GO; GO:0004722; P:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
DR KW Hydrolase; Magnesium.
SQ SEQUENCE 319 AA; 34477 MW; 0BD228603E34CFB0 CRC64;

Query Match 17.8%; Score 348; DB 10; Length 319;
Best Local Similarity 36.6%; Pred. No. 1.3e-21;
Matches 97; Conservative 45; Mismatches 89; Indels 34; Gaps 10;

Qy 96 GCASQICKRKENED----RFDAQLTDEVLYFVYDGHGGPAAADYCHTHMEKIMDL 151
Db 35 GYASSPGKSSMEDFYETRIDGVE-GEVVGILFGVDFDGHGGAAYVVKQL---FSLIK 90
Qy 152 KEKNLETLTLAFLDKAFSSHARLSADATLLTSGTTATVALLRDGIELV 203
Db 91 HPK-----FISDTKSAIAEAYHTDSEFLKSENTQNRDAGSTASTAIL-VGDRLLV 140
Qy 204 ASVGDRAILCRKPKMKLTIDHTPERKDEKRIKCGGFVAVNSLGGQPHVNGRLAMTRS 263
Db 141 ANVGDSRAVICRGGEATAVSRDKPKQSDERQIEDAGGFVWV--AGTWRVGGVLAWSRA 198
Qy 264 IGDLDLKTSGVIAEPETKRIKLHHADDS--FLVLTGGINFMVNSQEIICDFVNOCHD 321
Db 199 FGDKLLK-QYVVADEP---IQEEVVDSSLEFLILASDGLWDAFNSAEAVTFKPIQDTEE 254
Qy 322 AAHAHTEQAIQYGTEDNSTAVVVPFGAMGKYKNS 346
Db 255 AAKLMQEAQYRGSADNITCVVVR 279

RESULT 15
Q8H610 PRELIMINARY; PRT; 388 AA.
AC Q8H610;
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01-MAR-2003 (TRENBLrel. 23, Created)
01-MAR-2003 (TRENBLrel. 23, Last sequence update)
01-OCT-2003 (TRENBLrel. 25, Last annotation update)
Putative DNA-binding protein phosphatase 2C.
OSJNBA0035103.17.
Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriactoidae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, BAC
clone:OSJNBA0035103.17";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003019; BAC2243.1; -;
DR GO; GO:0008287; C:protein serine/threonine phosphatase complex; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0004722; F:protein serine/threonine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR00222; PP2C.
DR InterPro; IPR01932; PP2C-like.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
KW DNA-binding.
KW DNA-binding.
SQ SEQUENCE 388 AA; 42397 MW; B614776245AF9D77 CRC64;

Query Match 17.8%; Score 346.5; DB 10; Length 388;
Best Local Similarity 32.6%; Pred. No. 2.3e-21;
Matches 94; Conservative 55; Mismatches 98; Indels 41; Gaps 10;

Qy 82 KYGPIPKISLENVGCSAQIGKRENE-----RDFPAQLTDEVLYFAVYDGHG 130
Db 84 KSGNFVFN-----RSGDWSDIGRQYMEDTHVCITDLAKNFGQSVNDNEAISFYGVFDGHG 140

Qy 131 GPAAADFCHTHMEKCIIMDLPKENKLTLLTAFLEIDKAFSSHARLSADATLLTSGTTA 190
Db 141 GKDAHFVRDLPLIIVEDADFPLELEKVVRSFVHADNQFAK-----TTLSSGTTA 192

Qy 191 TVALLRDIELVVASGDSRAILCRKPKMKLTIDHTPERKDEKRIKCGGFVAVNSLG 250
Db 193 LTAMI-FGRTILLIANAGDRAVLSCGTATEMSVDHRCPSLSEKLRVESLGGYV-----D 246

Qy 251 QPHVNGRLAMTRSGIDLDEL---KTSG---VIAEPETKRIKLHADDSEFLVLTDTGINF 302
Db 247 DGYLNGLLGVTRAUGDHLGKMEAGNPGGFLSAPELQMITL-TKDDEFLIGSDGIWD 305

Qy 303 MVNSQEICDF---VNOCHDPNEAAHAHTQAIQYGTEDNSTAVVVPF 346
Db 306 VFSNQNVVDFARRLQEHNDVKSCCRIVEEAKRGATDNLTAVLVSF 353

Search completed: October 12, 2004, 06:02:43
Job time : 105 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 22 Seconds
(without alignments)
880.459 Million cell updates/sec

Title: US-10-716-488-2

Perfect score: 1951

Sequence: 1 MSTAALITLVRSGNQVRR.....KNSINFSSRFSSQGRWA 372

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	354.5	18.2	423	1 P2C2_ARATH	O04719 arabidopsis
2	338	17.3	434	1 P2C1_ARATH	P49597 arabidopsis
3	325	16.7	281	1 P2C1_YEAST	P35182 saccharomyc
4	321.5	16.5	347	1 P2C1_SCHPO	P40371 schizosacch
5	319.5	16.4	390	1 P2CB_RAT	P35815 rattus norv
6	310.5	15.9	383	1 P2C4_SCHPO	O14156 schizosacch
7	307.5	15.8	382	1 P2CA_BOVIN	O62829 bos taurus
8	307.5	15.8	382	1 P2CA_HUMAN	P35813 homo sapien
9	307.5	15.8	390	1 P2CB_MOUSE	P36993 mus musculu
10	306.5	15.7	382	1 P2CA_MOUSE	P49443 mus musculu
11	306.5	15.7	382	1 P2CA_RABIT	P35814 oryctolagus
12	306.5	15.7	382	1 P2CB_RAT	P20650 rattus norv
13	306.5	15.7	414	1 P2C3_SCHPO	Q09173 schizosacch
14	305	15.6	370	1 P2C2_SCHPO	Q09172 schizosacch
15	300.5	15.4	300	1 P2C2_PART	P49444 paramecium
16	297.5	15.2	387	1 P2CB_BOVIN	O62830 bos taurus
17	290.5	14.9	454	1 FEM2_HUMAN	P49593 homo sapien
18	282.5	14.5	479	1 P2CB_HUMAN	O75688 homo sapien
19	281	14.4	399	1 P2C4_ARATH	P49598 arabidopsis
20	279	14.3	406	1 P2C2_LEICH	P36992 leishmania
21	278	14.2	356	1 P2C2_CAEEL	P49596 caenorhabdi
22	264	13.5	450	1 FEM2_RAT	Q9wv77 rattus norv
23	264	13.5	464	1 P2C3_YEAST	P39966 saccharomyc
24	260	13.3	468	1 P2C3_YEAST	P34221 saccharomyc
25	228.5	11.7	542	1 P2CQ_MOUSE	O61074 mus musculu
26	226.5	11.6	491	1 P2C1_CAEEL	P49595 caenorhabdi
27	226	11.6	546	1 P2CG_HUMAN	O15355 homo sapien
28	223	11.4	543	1 P2CG_BOVIN	P79126 bos taurus
29	219	11.2	605	1 P2CD_HUMAN	O15297 homo sapien
30	218	11.2	598	1 P2CD_MOUSE	Q9qz67 mus musculu
31	216	11.1	388	1 P2C3_ARATH	P49599 arabidopsis
32	206.5	10.6	1839	1 CYAA_SACKL	P23466 saccharomyc
33	204	10.5	2026	1 CYAA_YEAST	P08678 saccharomyc

ALIGNMENTS

RESULT 1

ID	P2C2_ARATH	STANDARD;	PRT;	423 AA.
AC	O04719;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Protein phosphatase 2C ABI2 (EC 3.1.3.16) (PP2C) (Abscisic acid-insensitive 2).			
GN	ABI2 OR AT5G57050 OR MEM17.19.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsi.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia, and cv. Landsberg erecta;			
RX	MEDLINE=97308526; PubMed=9165752;			
RA	Leung J., Merlot S., Giraudat J.;			
RT	"The Arabidopsis ABSCISIC ACID-INSENSITIVE2 (ABI2) and ABI1 genes encode homologous protein phosphatases 2C involved in abscisic acid signal transduction."			
RL	Plant Cell 9:759-771(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Landsberg erecta;			
RX	Rodriguez P.L., Grill E.;			
RA	Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE=20181125; PubMed=10718197;			
RA	Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC clones."			
RL	DNA Res. 7:31-63(2000).			
CC	-!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.			
CC	-!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein + phosphate.			
CC	-!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).			
CC	-!- SIMILARITY: Belongs to the PP2C family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch .			
CC	EMBL; Y08966; CAA70163.1; -			
DR	EMBL; Y08965; CAA70162.1; -			
DR	EMBL; Y11840; CAA72338.1; -			

P38089 saccharomyc
P25646 saccharomyc
P49594 caenorhabdi
Q01513 podospora a
P49606 ustilago ma
Q15750 homo sapien
Q01631 neurospora
P35816 bos taurus
P46014 arabidopsis
O88483 rattus norv
Q9P2J9 homo sapien
Q9P0J1 homo sapien

34 202.5 10.4 393 1 P2C4_YEAST
35 194.5 10.0 442 1 FEM2_YEAST
36 192 9.8 449 1 FEM2_CAEEL
37 181.5 9.3 2145 1 CYAA_PODAN
38 175.5 9.0 2493 1 CYAA_USMA
39 170.5 8.7 504 1 TAB1_HUMAN
40 169 8.7 2300 1 CYAA_NEUCR
41 164.5 8.4 538 1 PDP1_BOVIN
42 159 8.1 581 1 KAPP_ARATH
43 153.5 7.9 538 1 PDP1_RAT
44 150.5 7.7 529 1 PDP2_HUMAN
45 149.5 7.7 538 1 PDP1_HUMAN

DR EMBL; AB024035; BAA7035.1; --
 DR HSP; P35813; 1A60.
 DR InterPro; IPR001532; P2C-like.
 DR InterPro; IPR000222; P2C.
 DR Pfam; PF00481; P2C; 1.
 DR SMART; SMO0331; P2C SIG; 1.
 DR SMART; SMO0332; P2C; 1.
 DR PROSITE; PS01032; P2C; 1.
 KW Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
 FT CA BIND 70 81 EF-HAND (POTENTIAL)
 SQ SEQUENCE 423 AA; 46306 MW; 67CAAC76DAS31A71 CRC64;
 Query Match 18.2%; Score 354.5; DB 1; Length 423;
 Best Local Similarity 30.6%; Pred. No. 3.7e-22;
 Matches 99; Conservative 51; Mismatches 99; Indels 75; Gaps 12;
 QY 96 GCASQIGRKENEDRFD-----FAQLTDEVL-----YFAYVDGCGPAAA 135
 DB 114 GVSICGRPEWDSVSTIPFLQVSSSLDGRVTNGFNPHLSAHPFGVYDGHGGSQA 173
 QY 136 DFCHEKMEKIMDLLPKK-----NLETLTLAFLIEDIDKAFSHARLSADATLL 184
 DB 174 NYCERMHALTEIVKEKPEFGDGTWQEKWKALFNSFMRVDSSETETVAHAPE----- 228
 QY 185 TSGTATVALRDGIELVWASVGSRAILCRKPKMLTIDHTPERKDEKERIKCGG-F 243
 DB 229 TVGSTVVAVFP-THIFVANGDSRAVLGRGKTPPLSLSDPDRDDEAR-EAAGKV 287
 QY 244 VAMNSLGGPHVNGRLATRSIGDLDTKTSVIAPE---TKRIKLHADDSEFLVLTDDGI 300
 DB 288 IRWNG---ARVFGVLMSRISGDRYLKPS-VIPDPVTSVRRVK-----EDDCILASDGL 339
 QY 301 NFMVNSQICDFVQ-----CHDPN-----EAAHVAITEQAIQYG 334
 DB 340 WDVNTNEVCDLARKILLWHKKNAMAGEALLPAEKREGKDPAAASAAYLSKMLQKG 399
 QY 335 TEDNSTAVVPFGAWGVKNSIN 358
 DB 400 SKDNISVVVDLKGIRAFKSKSLN 423
 RESULT 2
 P2C1 ARATH STANDARD; PRT; 434 AA.
 AC P48597; Q43717; Q94C87;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Protein phosphatase 2C AB11 (EC 3.1.3.16) (P22C) (Abscisic acid-insensitive 1).
 GN AB11 OR AT4G26080 OR P20B18.190.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANT ASP-180.
 RC STRAIN=cv. Landsberg erecta;
 RX MEDLINE=94255767; PubMed=8197457;
 RA Meyer K., Leube W.P., Grill E.;
 RT "A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis thaliana";
 RL Science 264:1452-1455(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Leaf;
 RX MEDLINE=95007759; PubMed=7923358;
 RA Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
 RT "The A. thaliana disease resistance gene RPS2 encodes a protein containing a nucleotide-binding site and leucine-rich repeats";
 RL Cell 78:1089-1099(1994).
 RN [3]

RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia; TISSUE=Leaf;
 RX MEDLINE=94255766; PubMed=7910981;
 RA Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F., Giraudat J.;
 RT "Arabidopsis ABA response gene AB11: features of a calcium-modulated protein phosphatase";
 RL Science 264:1448-1452(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Pohl K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Mayer T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N., Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Reichert B., Portetelle D., Zimmermann W., Wedler H., Bancroft I., Vos P., Hoheisel J., Zimmermann W., Boutry M., Schmidheini T., Langham S.-A., McCullagh B., Bilham L., Robben J., Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F., Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E., Keitzenegeer T., Bothe G., Ransperger U., Hilbert H., Braun M., Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., Mooljman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., Berner S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., De Keyser A., Buysshaert C., Gielens J., Villarroel R., De Clercq R., Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S., Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Pettett A., Rajandream M.A., Lyne M., Benes V., Rehnemann S., Borkova D., Bloeker H., Scharfe M., Grimm M., Loehnert T.-H., Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., Neumann S., Argüioy A., Vitale D., Liguori R., Piravandi E., Massenot O., Quigley F., Clabaud G., Muendlein A., Felber R., Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E., Gibbons T., Weber N., Vandenbol M., Bagues M., Terol J., Torres A., Perez-Perez A., Fumelle B., Bent E., Johnson S., Tacon D., Jesse T., Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bielke C., Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K., Parnell L., Dedhia N., Gnoj L., Schutz K., Huang B., Spiegel L., Sekhon M., Murray J., Sheer P., Cordes M., Abu-Thaideh J., Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J., Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D., Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K., Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.W., Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D., Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C., Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R., Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S., Granat S., Shohdy N., Hasegawa A., Hamed A., Lodhi M., Johnson A., Chen E., Marra M.A., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana";
 RL Nature 402:769-777(1999).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=22954850; PubMed=14593172;
 RA Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J., Cheuk R.F., Yamada K., Lim J., Dale J.M., Kim C.J., Nguyen M., Pham P.K., Yu G., Southwick A.M., Wu H.C., Kim C.J., Lam B., Sakano H., Wu T., Yu G., Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Lee J.M., Toriumi M.J., Chan M.M., Tang C.C., Banno F., Bowser L., Brooks S.Y., Carninci P., Arakawa T., Ban H., Banno F., Bowser L., Brooks S.Y., Carninci P., Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F., Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M., Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J., Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T., Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Empirical analysis of transcriptional activity in the Arabidopsis
 RL genome";
 CC Science 302:842-846(2003).
 CC -!- FUNCTION: Involved in abscisic acid (ABA) signaling pathway.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC
 DR EMBL; X78886; CAA55484.1; -;
 DR EMBL; U12856; AAB50237.1; -;
 DR EMBL; X77116; CAA54383.1; -;
 DR EMBL; AL049483; CAB39673.1; -;
 DR EMBL; AL161564; CAB79463.1; -;
 DR EMBL; AY035073; AAK59578.1; -;
 DR PIR; T04263; T04263.
 DR HSSP; P35813; 1A6Q.
 DR InterPro; IPR002048; EF-hand.
 DR InterPro; IPR001932; PP2C-like.
 DR InterPro; IPR000222; PP2C.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS00018; EF_HAND; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydroxylase; Magnesium; Manganese; Multigene family; Calcium-binding.
 FT CA BIND 93 104 EF-HAND (POTENTIAL).
 FT DOMAIN 417 420 POLY-VAL.
 FT VARIANT 180 180 G -> D (WILTY PHENOTYPE AND ABA-
 FT INSENSITIVE SEED GERMINATION AND GROWTH).
 FT CONFLICT 24 24 G -> R (IN REF. 5).
 FT CONFLICT 105 105 I -> V (IN REF. 1).
 FT SEQUENCE 434 AA; 47505 MW; 4A4C54F04195F572 CRC64;
 SQ
 Query Match 17.3%; Score 338; DB 1; Length 434;
 Best Local Similarity 30.9%; Pred. No. 9.3e-21;
 Matches 100; Conservative 46; Mismatches 98; Indels 80; Gaps 12;
 QY 96 GCASQIGKKKENED-----RDFALQTLDEVLYFAYVDHGHPAARD 136
 DB 130 GFTSICGRPEMEDAVSTIPFLQSSGMLDGRFDPQSAH---FFGYDGHGGSQVAN 186
 QY 137 FCHTHMEKIMDLLPKEKSL-----ETLLTFLAFLDKAFSSHARLSADATLLT 185
 DB 187 YCERHMLALAEIAKEKPMCDGTWLKWKKALFNSFLRVDSEIESVAP-----ET 239
 QY 186 SGTATVALLRGIEVLVAVSGDSRAILCRKGKPKMLTDHTPERKDEKERIKKCG-FV 244
 DB 240 VGSTSVAVVFPB-HIFVANCDSRAVLCKRGKTALPLSLVDHKPDREDEAARTEAAGGKY 298
 QY 245 ANNSLQPHNGFLANTRISGLDLKTSGLVIAEPE---TKRIKLHHADESFLVLTLDGIN 301
 DB 299 QMNG-----ARVFGVLAMRSRIGRDLKPS-IIPDPEVTAVRKV-----EDDCILASDGVW 350
 QY 302 FMVNSQIEICDFVQV-----CHDPN-----EAAHAYTEQAIQVQ 334
 DB 351 DVMTDEACEMARKILLWKKHKNVAGDASLLADERRKSGKDPAAAMAAEYLSKLAIQRG 410
 QY 335 TEDNSTAVVVVFPGAWGKYKNSIN 358
 DB 411 SKDNISVVVVDLKPRLKSKPLN 434

RESULT 3

P2C1 YEAST STANDARD; PRT; 281 AA.
 AC P35182;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Protein phosphatase 2C homolog 1 (EC 3.1.3.16) (P22C-1).
 GN PTC1 OR TPD1 OR YDJ006W OR D2925.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=93360976; PubMed=8395005;
 RX Maeda T., Teai A.Y.M., Saito H.;
 RT "Mutations in a protein tyrosine phosphatase gene (PTP2) and a
 RT protein serine/threonine phosphatase gene (PTC1) cause a synthetic
 RT growth defect in Saccharomyces cerevisiae.";
 RL Mol. Cell. Biol. 13:5408-5417(1993).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=94254822; PubMed=8196609;
 RX Robinson M.K., van Zyl W.H., Phizicky E.M., Broach J.R.;
 RT "TPD1 of Saccharomyces cerevisiae encodes a protein phosphatase
 RT 2C-like activity implicated in tRNA splicing and cell separation.";
 RL Mol. Cell. Biol. 14:3634-3645(1994).
 RL [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=S288C / AB972;
 RX Murphy L., Richards C., Gentles S., Harris D., Barrall B.G.,
 RA Rajadream M.A.;
 RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE OF 167-281 FROM N.A.
 RP STRAIN=S288C / AB972;
 RA Murphy L., Richards C., Gentles S., Harris D., Barrall B.G.,
 RA Rajadream M.A.;
 RT Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: It has a serine and a weak tyrosine phosphatase activity
 CC with ratios of serine to tyrosine phosphatase activity as high as
 CC 200:1. It is essential for growth or germination at 37 degrees
 CC Celsius. May have a role in the heat shock response. Involved in
 CC tRNA splicing and cell separation.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions. Manganese is
 CC about 20 times more efficient than magnesium.
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC
 DR EMBL; L14593; AAA34920.1; -;
 DR EMBL; Z48432; CAA88353.1; -;
 DR EMBL; Z74054; CAA98562.1; -;
 DR EMBL; Z48008; CAA88055.1; -;
 DR PIR; S41854; S41854.
 DR HSSP; P35813; 1A6Q.
 DR GerMOnline; 140248; -;
 DR SGD; S0002164; PTC1.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0005634; C:nucleus; IDA.
 DR GO; GO:0015071; F:protein phosphatase type 2C activity; IDA.
 DR GO; GO:0000001; P:mitochondrion inheritance; IMP.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.
 DR GO; GO:0006970; P:response to osmotic stress; IGI.
 DR GO; GO:0006388; P:tRNA splicing; IMP.
 DR InterPro; IPR001932; PP2C-like.

Db 228 VQN-----RINGVLAVTRALGDTYKLKL-VSAHPTTETRIWNGHDEPFIACDGLWDVV 281

QY 305 NSQEIICDFNQCHDFNEAAHVAHQIAIQGTEDNSTAVVV 344

Db 282 SDOEAVDFVRNFVSPREAAVRLVEFALKRLSDNITCIVV 321

RESULT 5

P2CB_RAT

ID P2CB_RAT STANDARD; PRT; 390 AA.

AC P35815; Q64046;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (1A)

DE (Protein phosphatase 1B)

GN PPMIB OR PPMIB OR PP2C2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Liver;

RX MEDLINE=92201367; PubMed=1312947;

RA Wenk J., Trompeter H.-I., Pettrich K.-G., Cohen P.T.W., Campbell D.G.,

RA Mieskes G.;

RT "Molecular cloning and primary structure of a protein phosphatase 2C

RT isoform";

RL PDBS Lett. 297:135-138 (1992).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Brain;

RX MEDLINE=95169115; PubMed=7532404;

RA Schafer K., Braun T.;

RT "Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+

RT dependent protein phosphatase beta";

RL Biochem. Biophys. Res. Commun. 207:708-714 (1995).

CC -!- FUNCTION: Enzyme with a broad specificity.

CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +

CC phosphate.

CC -!- COFACTOR: Moner (2 magnesium or manganese ions (By similarity)).

CC -!- SUBUNIT: Monomer (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist. Isoforms appear to

CC differ in their C-terminus;

CC Name=1; Synonyms=Beta-1;

CC Name=2; Synonyms=Beta-MPP;

CC IsoId=P35815-1; Sequence=displayed;

CC IsoId=P35815-2; Sequence=VSP_005093;

CC -!- SIMILARITY: Belongs to the PP2C family.

CC

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DR EMBL; S90449; AAB21898.1; -

DR EMBL; S74572; AAB33430.1; -

DR PIR; JC2524; JC2524.

DR PIR; S20392; S20392.

DR HSSP; P35813; 1A6Q.

DR InterPro; IPR001932; PP2C-like.

DR InterPro; IPR000222; PP2C.

DR Pfam; PF00481; PP2C.1.

DR SMART; SM00331; PP2C_SIG.1.

DR SMART; SM00332; PP2CC.1.

DR PROSITE; PS01032; PP2C.1.

KW Hydrolase; Magnesium; Manganese; Multigene family;

KW Alternative splicing.

FT METAL 37 MANGANESE 1 (BY SIMILARITY).

FT METAL 38 MANGANESE 1 (BY SIMILARITY).

FT METAL 60 MANGANESE 1 AND 2 (BY SIMILARITY).

FT METAL 243 MANGANESE 2 (BY SIMILARITY).

FT METAL 286 MANGANESE 2 (BY SIMILARITY).

FT VARSPLIC 379 390 GAGLEDSLVAL -> FYQPSTPYSDNVSYEWQT (in isoform 2).

FT /FTId=VSP_005093.

SQ SEQUENCE 390 AA; 42889 MW; DL47615EC2FA140B CRC64;

Query Match 16.4%; Score 319.5; DB 1; Length 390;

Best Local Similarity 31.6%; Pred. No. 2.9e-19;

Matches 94; Conservative 48; Mismatches 108; Indels 47; Gaps 10;

QY 88 PKISLENV-----GCASQISQIKRKENEDR-----PDFAQLTDEVLYFAVYDGHGQFAA 134

Db 8 PTEKKNHAGAGNGLRYGLSSMQWRVEMEDAHAVVGIPIHGLEDSFFAVYDGHAGSRV 67

QY 135 ADFCHTHM-----EKIMDLPEKKNLETLTFLAFLDKAFSSHARLSADA 181

Db 68 ANYCSTHLEHITTNEDFRAADKSGFALEPVENVTGIRTGFLKIDVYMRNFSDLRNG- 126

QY 182 TLLTSGTATVALLRDGIELVVASVGSRAILCRKGPMLKLTIDHTPERKDEKERIKKG 241

Db 127 -MDRSGSTA-VGVMISPTHYFINGDSRAVLCRNGQVCFSTQDKPCNPKMERIQNAG 184

QY 242 GFVAWNSIQGHVNGRLAMTRSIGDLDLK-----TSGVIA-EPETKRKIKLHHADDSFL 293

Db 185 G-----SWMIQRYNGSLAVSRALGDYDKVCDGKGPTEQLVSPPEYVEI-LRAEEDFV 238

QY 294 VLTDTGINFMVNSORICDFNQ-----CHDPNEAAHVAHQIAIQGTEDNSTAVVVVF 346

Db 239 VLACDGIWDVMSNEELCEFYNSRLVSDLENVGVNVDVTLCHKGRDNMSIVLCVF 295

RESULT 6

P2C4_SCHPO

ID P2C4_SCHPO STANDARD; PRT; 383 AA.

AC O14156; Q9UR02;

DT 15-JUL-1998 (Rel. 36, Created)

DT 26-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Protein phosphatase 2C homolog 4 (EC 3.1.3.16) (PP2C-4).

GN P1C4 OR SPAC48.03C.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RN [1]

RP SEQUENCE FROM N.A., SUBUNIT, SUBCELLULAR LOCATION, AND FUNCTION.

RC STRAIN=972;

RX MEDLINE=99365157; PubMed=10436019;

RA Gaits P., Russell P.;

RT "Vacuole fusion regulated by protein phosphatase 2C in fission

RT yeast";

RL Mol. Biol. Cell 10:2647-2654 (1999).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RX MEDLINE=21848401; PubMed=11859360;

RA Wood V., Guillermo R., Rajandream M.A., Lyne R., Stewart A.,

RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA Moorey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Stevens S.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Weiler H., Mambutt R., Purrelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RA "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880(2002).
 CC -!- FUNCTION: Has a role in the regulation of vacuole fusion.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: MEMBRANE-BOUND. VACUOLAR.
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC EMBL; AF140285; AAD27651.1; --
 CC EMBL; Z98762; CAB58554.1; --
 CC F1; T38772; T38772.
 CC GeneDB Spombe; SPAC4A8.03c; --
 CC InterPro; IPR001932; PP2C-like.
 CC InterPro; IPR00222; PP2C.
 CC Pfam; PF00481; PP2C; 1.
 CC SMART; SM00331; PP2C_SIG; 1.
 CC SMART; SM00332; PP2C; 1.
 CC PROSITE; PS01032; PP2C; 1.
 CC Hydrolase; Magnesium; Manganese; Membrane; Multigene family.
 KW METAL 92 92 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 308 308 MANGANESE 2 (BY SIMILARITY).
 FT METAL 347 347 MANGANESE 2 (BY SIMILARITY).
 FT METAL 363 363 MANGANESE 2 (BY SIMILARITY).
 SEQUENCE 363 AA; 43569 MW; 85E00C2BDAE4B9BF CRC64;
 Query Match 15.9%; Score 310.5; DB 1; Length 383;
 Best Local Similarity 28.5%; Pred. No. 1.6e-18;
 Matches 93; Conservative 52; Mismatches 118; Indels 63; Gaps 10;
 QY 86 PIPKSL---ENVGASQIGKRNEDRPFADLT-----DEVLYFAVYDGHGPPA 133
 Db 39 PYLKISMKAPQSGLCTARGDSFTNQDRMAYGYVNLKDTTDRDSPFFGLFDGSGTE 98
 QY 134 AADFCHTHMEKCI--MDLLPKKKNLETL-----159
 Db 99 CSEFLSTNLGIIINQDINDTEKILKEVSHVSGVGMAGLKPPFLRTVLQSRDEDLWRAR 158
 QY 160 LTLAFLETDKAF--SSHARLSADATLLTSGTTATVALI-----RDGIELVVASVGD 208
 Db 159 LYSFLQADMVLYNARSPDSAV--PGAVGTVAITTSKNLSYVESDSYIIHLAVGD 216
 QY 209 SRAILC--RKGPVKMLTIDHTPERKDEKIRIKCGGFVAMNSLQGPVNGKRLAMTRISGD 266
 Db 217 TRALLCDSTRGRLHRTFQHPADVEARLRLRYNMGFSRDSFGQKRF--AWVANTRSFGD 275
 QY 267 -LDLKTSGVIAEPETKILHADDSEVLVTTGTFNFWNSQELICDPVNOCHPNEAHA 325
 Db 276 GYLUKUGVNAEPOLTSIHSURDWSFLTLLSDGITDVVSDDEVDVLIKLSESPPQAANN 335
 QY 326 VTEQAIQYGTEDNSTAVVVPFGAMGX 351

Db 336 IIRYAQNVGAVDITCLVVRVLPFGMKX 361
 RESULT 7
 P2CA_BOVIN STANDARD; PRT; 382 AA.
 ID P2CA_BOVIN
 AC 062829;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha).
 GN PPM1A.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 RN NCBI_TaxID=9913;
 RX [1]_TaxID=9913;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Retina;
 RC MEDLINE=98146173; PubMed=9486768;
 RA Klump S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
 RT "Protein phosphatase type-2C isozymes present in vertebrate retinae:
 RT purification, characterization, and localization in photoreceptors.";
 RL J. Neurosci. Res. 51:328-338(1998).
 CC -!- FUNCTION: Enzyme with a broad specificity.
 CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
 CC phosphate.
 CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SIMILARITY: Belongs to the PP2C family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; A005457; CAA06554.1; --
 CC HSP; P35813; IAGQ.
 CC InterPro; IPR001932; PP2C-like.
 CC InterPro; IPR00222; PP2C.
 CC Pfam; PF00481; PP2C; 1.
 CC SMART; SM00331; PP2C_SIG; 1.
 CC SMART; SM00332; PP2C; 1.
 CC PROSITE; PS01032; PP2C; 1.
 CC Hydrolase; Magnesium; Manganese; Multigene family.
 KW METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
 FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
 SEQUENCE 382 AA; 42529 MW; A7163FA0E7E21C2 CRC64;
 Query Match 15.8%; Score 307.5; DB 1; Length 382;
 Best Local Similarity 31.0%; Pred. No. 2.8e-18;
 Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;
 QY 88 PKISLNV-----CCASQIGKRNEDR-----PDFAQLTDEVLYFAVYDGHGPPA 134
 Db 8 POMEKXNAQGGNGRLYGLSSNQGRVEMEDAHAVIGLPSGLTWSFFAVYDGHASQV 67
 QY 135 ADFCHTHMEKIMDL-----LPKRNLETLTLTFLAFLEIDK--AFSSHARLSADATLL 184
 Db 68 AKYCCHELLDHTNNQDFKGSAGAPSVENVKNGIRTGTFLEIDHMRVMSEKKGAD--- 123
 QY 185 TSGTATTATVALLRDGIELVVASVGSRAILCRKGFPMKLTIDHTPERKDEKIRIKCGGFV 244
 Db 124 RSGSTA--GVGLISPOHTYFINGDSRGLLCRNRYVFTQDHKPSNPLEKRIQAGG-- 180
 QY 245 AMNSLQGPVNGRLAMTRISIGDLK-----TSGVIA--EPETKRIKLHADDSEVLVLT 296

Db 181 ---SVMQIRVNGSLAVSRALGDFDKVHGKPTQLVSPPEVHDIERSEDDQFIILA 237
Qy 297 TGINFMVNSQICDFVQVQ-----CHDPNEAAHAYTEQAIQYGTEDNSTAVVVPF 346
Db 238 CDGIWDVNGNEELCDFVSRLEVTDDLEKVCNEVVDTCLYKGRDNMSVILICF 291

RESULT 8
P2CA HUMAN
ID P2CA HUMAN STANDARD; PRT; 382 AA.
AC P35813; 075551;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (P2C-alpha) (TA)
GN PPM1A OR PPM1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RX MEDLINE=92182001; PubMed=1311954;
RA Mann D.J., Campbell D.G., McGowan C.H., Cohen P.T.W.;
RT "Mammalian protein serine/threonine phosphatase 2C: cDNA cloning and
RT comparative analysis of amino acid sequences.";
RL Biochim. Biophys. Acta 1130:100-104(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-2).
RX MEDLINE=98372738; PubMed=9707433;
RA Takekawa M., Maeda T., Saito H.;
RT "Protein phosphatase 2Calpha inhibits the human stress-responsive p38
RT and JNK MAPK pathways.";
RL EMBO J. 17:4744-4752(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA-1).
RC TISSUE=Colon; PubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:15899-15903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RX MEDLINE=97157470; PubMed=9003755;
RA Das A.K., Helps N.R., Cohen P.T.W., Barford D.;
RT "Crystal structure of the protein serine/threonine phosphatase 2C at
RT 2.0-A resolution.";
RL EMBO J. 15:6798-6809(1996).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
CC -!- SUBUNIT: Monomer.
CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha-1;
CC IsoId=P35813-1; Sequence=Displayed;
CC Name=Alpha-2;
CC IsoId=P35813-2; Sequence=VSP_005085, VSP_005086;
CC -!- SIMILARITY: Belongs to the P2C family.
CC
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CC
CC EMBL; S8759; AAB21784.1; -;
CC EMBL; AF070670; AAC28354.1; -;
CC EMBL; BC026691; AAH26691.1; -;
CC PIR; S22423; S22423.
CC Genew; HGNC:9275; PPM1A.
CC MIN; 606108; -;
CC PDB; 1A6Q; 27-MAY-98.
CC GO; GO:0015071; F:protein phosphatase type 2C activity; TAS.
CC InterPro; IPR001932; P2C-like.
CC InterPro; IPR000222; P2C.
CC Pfam; PF00481; P2C; 1.
CC SMART; SM00331; P2C_SIG; 1.
CC SMART; SM00332; P2C_C; 1.
CC PROSITE; PS01032; P2C; 1.
KW Hydroxylase; Magnesium; Manganese; Multigene family;
KW Alternative splicing; 3D-structure.
FT METAL 37 37 MANGANESE 1.
FT METAL 38 38 MANGANESE 1.
FT METAL 60 60 MANGANESE 1 AND 2.
FT METAL 239 239 MANGANESE 2.
FT METAL 282 282 MANGANESE 2.
FT VARSPLIC 318 324 EIIKKQG -> GGSFNKK (in isoform Alpha-2).
FT VARSPLIC 325 382 Missing (in isoform Alpha-2).
FT VARSPLIC 325 382 /FTId=VSP_005085.
FT VARSPLIC 325 382 /FTId=VSP_005086.
FT STRAND 9 19
FT TURN 20 21
FT STRAND 22 31
FT TURN 32 32
FT STRAND 38 46
FT STRAND 47 49
FT STRAND 50 62
FT TURN 66 80
FT HELIX 81 81
FT TURN 83 86
FT HELIX 94 118
FT TURN 119 120
FT STRAND 126 127
FT STRAND 129 134
FT STRAND 138 144
FT STRAND 148 153
FT TURN 154 155
FT STRAND 156 160
FT TURN 166 167
FT TURN 169 177
FT TURN 178 179
FT STRAND 182 183
FT TURN 184 185
FT STRAND 186 187
FT TURN 188 190
FT STRAND 191 191
FT STRAND 195 195
FT STRAND 197 198
FT HELIX 200 202
FT TURN 206 207
FT TURN 210 212
FT HELIX 216 216
FT STRAND 220 225

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FT TURN 228 230
FT STRAND 231 237
FT HELIX 239 242
FT TURN 243 244
FT HELIX 247 258
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FT HELIX 264 277
FT TURN 278 279
FT STRAND 284 290
FT TURN 292 293
FT HELIX 299 319
FT HELIX 330 339
FT TURN 340 341
FT TURN 347 349
FT HELIX 350 354
FT HELIX 355 365
SQ SEQUENCE 382 AA; 42447 MW; D48EF508B4A76687 CRC64;

Query Match
Best Local Similarity 31.0%; Score 307.5; DB 1; Length 382;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;

QY 88 PKISLENV-----GCASQIGKREKEDR-----PDFALTDVLYFAVYDCHGGPAA 134
DQ 8 PMEKHNAGQGGNGRLYGLSSMOQGRVEMEDAHTAVIGLPSGLSWFFFAVYDGHAGSQV 67
QY 135 ADFCHTHMEKIMDL-----LPKEKNLETLTLTFLAFLDK--AFSSHARLSADATLL 184
DQ 68 AKYCCHELLDHTNNQDFKGSAGAPSVENVKNGIRGTGFLDEHWRVNSEKHCAD---- 123
QY 185 TSGTATVALRDGIELVAVSGSRALLCRKGPMLTIDHTPERKDEKERIKKCGGFV 244
DQ 124 RSGSTA-VGVLLSPQHTYFNCGRSGLLRKRRVHFFETQDKPSNPLEKRIQAGG-- 180
QY 245 AwnSLGQPHVNGRLAMTRISIGDLK-----TSGVIA-EPEPKRIKLHADDSDFLVLT 296
DQ 181 ---SVMIOVRNGSLAVSRALGDFDYKCVHGKGPTEQLVSPPEVHDIERSEDDQFIILA 237
QY 297 TDGNNFMVNSOIEICFVNQ-----CHDNEAAHAYTEQAIQVGTEDNSTAVVWPF 346
DQ 238 CDGIWDMNGNEELCDFVRSLREVTDDLEKVCNEVVDTCLYKGRSDNMSVLICF 291

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RESULT 9

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P2CB_MOUSE STANDARD; PRT; 390 AA.
AC P36993;
DT 01-JUN-1994 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (P2C-beta) (IA)
DE (Protein phosphatase 1B).
GN PPM1B OR PPM1B OR PPM1B OR PPM1B
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94099616; PubMed=8274020;
RA Terashima T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
RA Kato S., Terashima T., Kobayashi T., Takeuchi T., Tamura S.,
RA Tanaka O., Kondo H., Yamamoto H., Yamamoto H., Matsui Y.,
RT "Molecular cloning of a novel isotype of Mg(2+)-dependent protein
RT phosphatase beta (type 2C beta) enriched in brain and heart.";
RL Arch. Biochem. Biophys. 307:342-349(1993).
RN [2]
RP SEQUENCE FROM N.A. (BETA-3, BETA-4 AND BETA-5).
RX MEDLINE=95251388; PubMed=7733667;
RA Kato S., Terashima T., Kobayashi T., Ohnishi M., Sasahara Y.,
RA Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.,
RT "Molecular cloning and expression of mouse Mg(2+)-dependent protein
RT phosphatase beta-4 (type 2C beta-4).";

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RL Arch. Biochem. Biophys. 318:387-393(1995).
RN [3]
RP SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
RX TISSUE=Testis;
RX MEDLINE=94313028; PubMed=8038726;
RA Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
RT "Molecular cloning and expression of cDNAs encoding two isoforms of
RT protein phosphatase 2C beta from mouse testis.";
RL Biochem. Mol. Biol. Int. 32:773-780(1994).
RN [4]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SV;
RX MEDLINE=99398339; PubMed=10469137;
RA Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
RA Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
RT "Alternative promoters direct tissue-specific expression of the mouse
RT protein phosphatase 2C beta gene.";
RL Eur. J. Biochem. 263:736-745(1999).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Comment=Isoforms only differ in their C-terminus;
CC Name=Beta-1;
CC IsoID=P36993-1; Sequence=Displayed;
CC Name=Beta-2;
CC IsoID=P36993-2; Sequence=VSP_005089;
CC Name=Beta-3;
CC IsoID=P36993-3; Sequence=VSP_005090;
CC Name=Beta-4;
CC IsoID=P36993-4; Sequence=VSP_005091;
CC Name=Beta-5;
CC IsoID=P36993-5; Sequence=VSP_005092;
CC -!- TISSUE SPECIFICITY: Beta-1 is expressed ubiquitously; beta-2 is
CC expressed exclusively in brain and heart; beta-4 is expressed
CC exclusively in brain and intestine; beta-3 and beta-5 are
CC expressed exclusively in testis and intestine.
CC -!- SIMILARITY: Belongs to the P2C family.
CC -----
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CC EMBL; D17411; BAA04233.1; -
CC EMBL; D17412; BAA04234.1; -
CC EMBL; D45859; BAA08293.1; -
CC EMBL; D45860; BAA08294.1; -
CC EMBL; D45861; BAA08295.1; -
CC EMBL; U09218; AAB560442.1; -
CC EMBL; AB007798; BAA84471.1; -
CC EMBL; AB007794; BAA84471.1; JOINED.
CC EMBL; AB007795; BAA84471.1; JOINED.
CC EMBL; AB007796; BAA84471.1; JOINED.
CC EMBL; AB007797; BAA84471.1; JOINED.
CC PIR; I49016; I49016.
CC PIR; S65672; S65672.
CC HSP; P35813; I49Q.
CC MGD; MGI:101841; Ppm1b.
CC InterPro; IPR001932; P2C-like.
CC InterPro; IPR00222; P2C.
CC Pfam; PF00481; P2C; 1.
CC SMART; SM00331; P2C SIG; 1.
CC SMART; SM00332; P2CC; 1.
CC PROSITE; PS01032; P2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family;
CC Alternative splicing.

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FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 2 (BY SIMILARITY).
FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 286 286 MANGANESE 2 (BY SIMILARITY).
FT VARSPLIC 379 390 GAGDLEDSLVL -> VSLHLPFKYK (in isoform Beta-2).
FT VARSPLIC 379 390 /FTID=VSP 005089.
FT VARSPLIC 379 390 GAGDLEDSLVL -> FYQPSIAYSDNNVLL (in isoform Beta-3).
FT VARSPLIC 379 390 /FTID=VSP 005090.
FT VARSPLIC 379 390 GAGDLEDSLVL -> MADLSTICKPS (in isoform Beta-4).
FT VARSPLIC 379 390 /FTID=VSP 005091.
FT VARSPLIC 379 390 VAL -> FYQPSIAYSDNNVLL (in isoform Beta-5).
FT VARSPLIC 379 390 /FTID=VSP 005092.
FT SEQUENCE 390 AA; 42795 MW; 255C97B4276189FD CRC64;
Query Match 15.7%; Score 307.5; DB 1; Length 390;
Best Local Similarity 31.0%; Pred. No. 2.9e-18;
Matches 92; Conservative 48; Mismatches 110; Indels 47; Gaps 10;
QY 88 PKISLENV-----GCASQIGKRNEDR-----FDPAQLTDEVLYFAYVDGSGPAA 134
DB 8 PATEKHNAHAGNGLYRGLSSQGNRVEMEDAHAVGIPGLDNNWFFAYVDGHAGSRV 67
QY 135 ADPCHTHM-----SKCIMDLLPEKKNLETLTLAFLEIDKAFSHARLSADA 181
DB 68 ANVCSTHLEHTTWNEDFRAADKSGSALEPSVESVKTGRTGLKIDEMRNFSLRNG- 126
QY 182 TLLTSGTTATVALLRDGIELVAVSGDSRAILCRKQKPKMLTIDHTPERKDEKRIKCG 241
DB 127 -MDRSGSTA-VGMVSPTHNYFINCDSRAVLCRNGQVCFTQDKPCNPVEKERIQNAG 184
QY 242 GFVAMNSLQCPHNGVGLAMTRISGDLK-----TSGVIA-EPETKRIKLHADDNFL 293
DB 185 G-----SVMIQVNGSLAVSRALGDYKCVGKGTQELQVSPPEVVEI-VRAEDSFV 238
QY 294 VLTDTGINFWNSQELCDFVQ-----CHDPNEAAHVAITEQATQYCTEDNSTAVVVPF 346
DB 239 VLACDGIWDMGNEELCEFKRLEVSDDLNVNVCNMVVDTCCLKHGRDNNVVLVCF 295
RESULT 10
P2CA MOUSE STANDARD; PRT; 382 AA.
AC P4943;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Protein phosphatase 2C alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
GN PPM1A OR PPM1A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94333828; PubMed=8056349;
RA Kato S., Kobayashi T., Terasawa T., Ohnishi M., Sasahara Y.,
RA Kanamaru R., Tamura S.;
RT "The cDNA sequence encoding mouse Mg2+ -dependent protein phosphatase
alpha."
RL Gene 145:311-312(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Basak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Enzyme with a broad specificity.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.
CC -!- COFACTOR: Binds 2 magnesium or manganese ions.
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
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CC -----
CC EMBL; D28117; BAA05662.1; --
CC EMBL; BC008595; AA080595.1; --
CC F01; 153823; 153823.
CC HSP; P35813; 1A6Q.
CC MG; MG1:99878; Ppm1a.
CC InterPro; IPR001932; PP2C-like.
CC InterPro; IPR000222; PP2C.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC SMART; SM00332; PP2C; 1.
CC PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
FT SEQUENCE 382 AA; 42432 MW; DC206610E1583870 CRC64;
Query Match 15.7%; Score 306.5; DB 1; Length 382;
Best Local Similarity 31.0%; Pred. No. 3.4e-18;
Matches 91; Conservative 43; Mismatches 115; Indels 45; Gaps 10;
QY 88 PKISLENV-----GCASQIGKRNEDR-----FDPAQLTDEVLYFAYVDGSGPAA 134
DB 8 PATEKHNAHAGNGLYRGLSSQGNRVEMEDAHAVGIPGLDNNWFFAYVDGHAGSRV 67
QY 135 ADPCHTHMCKIMDL-----LPKEKNLETLTLAFLEIDK--AFSSHARLSADATLL 184
DB 68 AKYCCHELLDHTNNQDFRSGAGAPSVENVNGRTGFEIDEMRVNSEKKGAD---- 123
QY 185 TSGTTATVALLRDGIELVAVSGDSRAILCRKQKPKMLTIDHTPERKDEKRIKCGFV 244
DB 124 RSGSTA-VGVLTSPQHTYFINGDSRGLCRNRKVHFFTDHQPNSPLERIKRINAG-- 180
QY 245 AWWSLGQPHVNGRLAVTRISIGDLK-----TSGVIA-EPETKRIKLHADDNFLVIT 296
DB 181 ---SVMIQVNGSLAVSRALGDFYKCVGKGTQELQVSPPEVVDIERSEDDQFIILA 237
QY 297 TDGINFWNSQELCDFVQ-----CHDPNEAAHVAITEQATQYCTEDNSTAVVVPF 346
```


68 AYCEHLDHITNQDFKSGAGAPSVENKNGTGTGLEIDHEHMRVSEKKGAD----- 123
185 TSGTTATVALLRDGIELVAVGDSRAILCRKGPMLTIDHTPERKDEKRIKKCGFV 244
124 RSGSTA-VGVLSIPQHTFYNGDSRGLCRNRKVHFTQDKPSNPLEKERIQNAGG-- 180
245 AWNSLQGVHNGRLAMTSGIDLDL-----TSGVIA-EPETKRIKLHADDSEFLVLT 296
181 ---SVNIORVNGSLAVSALGDFDKYGVHGKPTQLVSPPEVHDIERSEDDQFILA 237
297 TDGINFMVNSOICDFVQ-----CHDPNEAAHVAITEQAIOYGTEDNSTAVVVF 346
238 CDGIWVNGNEBELCDFVSRLEVTDDLEKVCNEVVDTCLYKGRDNMSVILICF 291
RESULT 13
ID P2C3 SCHPO STANDARD; PRT; 414 AA.
AC Q09173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
GN PTC3 OR SPAC2G11.07C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=95163582; PubMed=7859738;
RA Shiozaki K., Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
RT kinase kinase homolog in the osmotic regulation of fission yeast.";
RL ENBO J. 14:492-502 (1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth I., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy S., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA Welter J., Vansteels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardet C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Sipakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RT Nature 415:871-880 (2002).
CC -!- FUNCTION: Has an important role in osmotic stability and cell
CC shape control. It may negatively regulate the osmosensing signal
CC transmitted through wsl map kinase.
CC -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC phosphate.

-!- COFACTOR: Binds 2 magnesium or manganese ions (By similarity).
CC -!- SUBUNIT: Monomer.
CC -!- SIMILARITY: Belongs to the PP2C family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L34882; AAA67321.1; -;
CC EMBL; Z54354; CAA91172.1; -;
CC PIR; T38573; S62462.
CC HSP; P35813; 1A6O.
CC GeneDB SPombe; SPAC2G11.07C; -;
DR InterPro; IPR001932; PP2C-like.
DR InterPro; IPR000222; PP2C.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_Sig; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 230 230 MANGANESE 2 (BY SIMILARITY).
FT METAL 279 279 MANGANESE 2 (BY SIMILARITY).
FT CONFLICT 196 196 K -> T (IN REF. 1).
SQ SEQUENCE 414 AA; 44856 MW; EBF3A416625A2B11 CRC64;
Query Match 15.7%; Score 306.5; DB 1; Length 414;
Best Local Similarity 33.1%; Pred. No. 3.8e-18;
Matches 97; Conservative 38; Mismatches 103; Indels 55; Gaps 12;
QY 96 GCASQIGKRNED-----RFDPAQLTDELYFAVYDGHGGPAAADPCHTHMEKIMDL 149
DB 25 GLSSMQGWRISMEDAHSAILSMCECAVKDPVDFVYDGHGGDKVAKWCSNLPQIL--- 81
QY 150 LPKKNLE-----TLTTLAFLEIDKAFSHARLSADATLLTSGTTATVALLRDGIELV 202
DB 82 ---EKNPDFQKGFVNALKSFLNADKAILDDQDQFHTD---PSGCTATV-VLRVGNKLY 133
QY 203 VASVGDGRAILCRKGPMLTIDHTPERKDEKRIKKCGFVAVNSLQGFHVNGRLAMTR 262
DB 134 CANAGDSRTVLGSGIAKPLSADHKPSNEAEKARICAGGFVDFG----RVNGNLALS 188
QY 263 SIGDLDLKTSGVIAEPETK-----RIKLHHA--DSSFVLTTDTGIMPVNSOICDFVN 314
DB 189 AIGDFEPEKSNL--EPEKQIVTALPDPVVVHVEITDDDEFVLACDGIWDCKTSQVIEFVR 246
QY 315 Q-----CHDPNEAAHVAITEQAIOYGT-----DNSTAVVVF-----GAWGK 351
DB 247 RGIVAGTSLEKIAENMDNCIASDTETTGCLCDNNTVCIVALLQENDKSANYK 299
RESULT 14
ID P2C2 SCHPO STANDARD; PRT; 370 AA.
AC Q09172;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
GN PTC2 OR SPCC1223.11.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.

DD
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K

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 12, 2004, 05:55:18 ; Search time 36 Seconds
(without alignments)
993.979 Million cell updates/sec

Title: US-10-716-488-2
Perfect score: 1951
Sequence: 1 MSTAAALTLVRSGNQVRR.....KNSEINFGRSFASGRWA 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: Pir1:*
2: Pir2:*
3: Pir3:*
4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	360	18.5	348	T50783	protein phosphatas
2	357	18.3	383	T48018	hypothetical prote
3	344.5	17.7	392	F84650	probable protein p
4	338	17.3	434	T04263	phosphoprotein pho
5	337.5	17.3	381	T03640	protein phosphatas
6	332.5	17.0	359	T52337	phosphoprotein pho
7	328	16.8	362	F84695	probable protein p
8	326	16.7	464	H95700	protein F12A21.5
9	325	16.7	281	S41854	phosphoprotein pho
10	322.5	16.5	239	T01361	probable protein p
11	322.5	16.5	816	T48123	hypothetical prote
12	322	16.5	511	F96752	protein phosphatas
13	321.5	16.5	347	A56058	phosphoprotein pho
14	320	16.4	355	H84643	probable protein p
15	319.5	16.4	389	T05095	hypothetical prote
16	319.5	16.4	390	S20392	phosphoprotein pho
17	319.5	16.4	397	JC3524	phosphoprotein pho
18	318.5	16.3	423	T48121	hypothetical prote
19	318	16.3	238	D96811	hypothetical prote
20	311.5	16.0	361	T45778	protein phosphatas
21	310.5	15.9	383	T38772	protein phosphatas
22	307.5	15.8	382	S22423	phosphoprotein pho
23	307.5	15.8	390	S65672	phosphoprotein pho
24	307.5	15.8	393	T49016	phosphoprotein pho
25	307.5	15.8	396	T02483	probable protein p
26	306.5	15.7	382	I53823	magnesium dependen
27	306.5	15.7	382	S22422	phosphoprotein pho
28	306.5	15.7	382	A32399	phosphoprotein pho
29	306.5	15.7	414	S62462	protein phosphatas

30	305	15.6	370	2	S54297	protein phosphatas
31	304	15.6	404	2	T00750	probable protein p
32	304	15.6	442	2	B86209	protein F22G5.22 l
33	301	15.4	357	2	T06308	protein phosphatas
34	301	15.4	1428	2	T13926	probable protein p
35	300.5	15.4	300	2	A55804	phosphoprotein pho
36	288.5	14.8	268	2	T04610	protein phosphatas
37	288	14.8	281	2	F86355	T1615.10 protein
38	287.5	14.7	242	2	T18588	probable protein p
39	285.5	14.6	290	2	E84591	probable protein p
40	285.5	14.6	380	2	E84748	phosphoprotein pho
41	281	14.4	399	2	S55457	phosphoprotein pho
42	279	14.3	406	2	A47492	hypothetical prote
43	278.5	14.3	405	2	F86206	probable protein p
44	278.5	14.3	514	2	D84584	protein T23F11.1 l
45	278	14.2	348	2	E88434	

ALIGNMENTS

RESULT 1

T50783
protein phosphatase 2C-like protein - Arabidopsis thaliana
N;Alternate names: protein T30N20_10
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 15-Jun-2001
C;Accession: T50783
C;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; Newe
submitted to the Protein Sequence Database, July 2000
A;Reference number: Z25240
A;Accession: T50783
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <BEV>
A;Cross-references: EMBL:AL365234
A;Experimental source: cultivar Columbia; BAC clone T30N20
C;Genetics:
A;Map position: 5
A;Introns: 27/2; 70/1; 103/1; 156/1; 185/1; 209/3; 234/3
A;Note: T30N20_10
C;Superfamily: human phosphoprotein phosphatase 1A

Query Match	18.5%;	Score 360;	DB 2;	Length 348;
Best Local Similarity	35.4%;	Pred. No. 1e-22;		
Matches	99;	Conservative	56;	Mismatches 89; Indels 36; Gaps 11;
QY	96	GCASQIGKRNEDRD--FAQLTDEVL-YFAYVDGGPAAADFCHTHMEKCIIMDLPK	152	
Db	35	GYASSAGKRSMDFFETRIDGNGEIVGLFVDGHHGARAAYVVRHL---	FSNLITH 91	
QY	153	EK---NLETLITLAFLEID---KAFSSHARLSADATLLTSGTTATVALLRDGIELVVAS	205	
Db	92	PKFISDTKSAITDAYNHTDSELLKSENHNR-----DAGSTASTAIL-VGDRLVVAN	142	
QY	206	VGDSRAILCRGPKMLTIDHTPERKDEKRIKCGGFVAVNSLGQFVNGRLAMTSIG	265	
Db	143	VGDSRAVISGGKAIVSRDHKPDQSDERERENAGGFVNW-----AGVLAVSAFG	194	
QY	266	DLDLKTSVIAEPETKIKLHHADS--FLVLITDGINFVNSOEICDFVNQCHDPNEAA	323	
Db	195	DLRLK-QYVVADPIQBEKI---DDTLFLLASDGLWDVFSNEAAVAMVKEVEDPDSA	250	
QY	324	HAVTEQAIQYGTENSTAVVPPFGAWGKYNKNSINFESR	363	
Db	251	KKLVGGAIKRGSADNITCVVVRVLEKKSSASSHSSSSK	290	

RESULT 2

T48018
hypothetical protein T17J13.220 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

```

QY 121 -LYFAYVDHGQFAADF-CHTHMEKCINDLLPKEKNLETLTLAFLEIDKAFSSHARLS 178
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 126 SAFYGVVDHGQGHAAEFACH-HIPRYIVEDQEFFSEINKVLSSAFLQDTDTAFLEACSLD 184

QY 179 ADATLLTSTTATVALLRGIELVVASVGDSSAILCRKGKPKMLTIDHTPERKDKERIK 238
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 185 GS---LASGTTALAAIL-FGRSLWANAGDCRAVLISROKATIEMRDRIKPMSSKERRIE 240

QY 239 KCGGFVAMNSLQPHVNGRLAMTRSGIDLDL-----KTSG-----VIAEPETKRIKLHHA 288
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 241 ASGCHVF-----DGYLNGQLNVARALGFHMGEMKKKKDGGDCGPLIAEPELMTTKLIE- 294

QY 289 DGSFLVLTTDGINFMVNSQIECDF-----VQCCHDPNEAAHVAVTBOAIQYGTEDNSTAVVV 344
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 295 EDEFLIIGDGVMDVFMFSQNAVDFARRRLQEHNDPVMGSKELVEEALKRKGSADNVTAVVV 354

RESULT 4
T04263
phosphoprotein phosphatase (EC 3.1.3.16) ABI1 - Arabidopsis thaliana
N;Alternate names: protein P20B18.190
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 08-Oct-1999
C;Accession: T04263; A54588
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F.X.
submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15263
A;Accession: T04263
A;Molecule type: DNA
A;Residues: 1-434 <BEV>
A;Cross-references: EMBL:AL049483
A;Experimental source: cultivar Columbia; BAC clone F20B18
R;Meyer, K.; Leube, M.P.; Grill, E.
Science 264, 1452-1455, 1994
A;Title: A protein phosphatase 2C involved in ABA signal transduction in Arabidopsis thal
A;Reference number: A54588; MUID:94255767; PMID:8197457
A;Accession: A54588
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-104, 'V', 106-434 <MEY>
A;Cross-references: GB:X78886; NID:G509418; PIDN:CAA55484.1; PID:G509419
C;Genetics:
A;Gene: ABI1
A;Map position: 4
A;Introns: 183/3; 280/3; 316/1
A;Note: P20B18.190
C;Keywords: phosphoric monoester hydrolase

Query Match 17.3%; Score 338; DB 2; Length 434;
Best Local Similarity 30.9%; Pred. No.1e-20;
Matches 100; Conservative 46; Mismatches 99; Indels 80; Gaps 12;

QY 96 GCASQIGKXKKNED-----RPFQAQLTDEVLYFAVYDGHGQPAAD 136
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 130 GFTSICGRRPEDAVSTIPFLQSSGSLDGRFDPOSAAH---FFGVYDGHGGSQVAN 186

QY 137 FCHTHMEKCINDLLPKEKNL-----ETLLTLAFLEIDKAFSGSHARLSADATLLT 185
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 187 YCERMRHLAAEEIAKEKPMLCDGDTWLKWKKALFNSFLRVDSEIESVAP-----ET 239

QY 186 SGTTATVALLRDGIELVVASVGDSSAILCRKGKPKMLTIDHTPERKDKERIKKCGG-FV 244
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 240 VGSTSVAVWFPS-HIFVANGCDGRAVLCKGTALPLSLVDHKHDPREDEAARIEAAGKVI 298

QY 245 AwnSLGQPHVNGRLAMTRSGIDLDLKTSGVIAEPE---TKRIKLHHA DDSFLVTTDGIN 301
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 299 QWNG---ARVFGVLAMNSISGDRIKPS-IIPDEVTA VRVK-----EDDCILIASGVW 350

QY 302 FMVNSQIECDFVQ-----CHDPN-----EAAHVTFOAIQYG 334
   ::::::::::::::::::::: : : : : : : : : : : : : : : : : : : : : : : :
Db 351 DWTDEEACEMARKRIILLWHKKNVAGDASILLADERRKEGKDPAAMGAAEYLSKLAIQRG 410

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Db      22  GQLDINTPD-----AVSDNSLASTMLOFVNIRSGS-----PADIG 58
QY      103  KKENED---RFD-----FAQLTDEVLYFAYDGHGGPAAADFCHTHWEKICMD--L 149
Db      59  PKYMEDESHRIDDLVSQGLSFLCPKPSAYGVDFDGGGSEAAAYVRENVMRFFEDVS 118
QY      150  LPKEKNL-----ETLLTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIEL 201
Db      119  FFEASELDEIFLEGVENCRRRAFFLADLADDCSIST-----SGTALTALVL-GRLL 172
QY      202  VVASVGDSSRAILCRKGKPMKLTIDHTPERKDEKERIKKCGGFVAVNSLGFPHVNGRLAMT 261
Db      173  LVANAGDCRAVLCKGGEAIDXSQHRPTYPEKRRVEELGGYV-----DDGYLNGVLVS 227
QY      262  RSIGDLDLK-----TSGVIAPEPKRIKLHADDSFLVLTDDGINFMVNSQEIcdfv--- 313
Db      228  RALGDWDMKLPKGSASPLISEPELRQIILTE-DDEFLIIGCDG:WDWISSQQAVSVIRWG 286
QY      314  -NOCHDPNEAAHAVTEQAIOYGTEDNSTAVVVPFGA 348
Db      287  LKRHDDPQSADLVNEALRHTIDNLTVIIVCFSS 322

RESULT 7
F84695
probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: F84695
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanKaken, S.E.; Unayam, L.; Tallon, J.
eaus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:reference number: A84420; MUID:20083487; PMID:10617157
A:Accession: F84695
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-362 <STO>
A:Cross-references: GB:AE002093; NID:G980397; PIDN:AAC95200.1; GSPDB:GN00139
C:Genetics:
A:Gene: Ac2g29380
A:Map position: 2
C:Superfamily: Arabidopsis thaliana hypothetical protein F7A7.220

Query Match 16.8%; Score 328; DB 2; Length 362;
Best Local Similarity 28.9%; Pred. No. 5,7e-20;
Matches 108; Conservative 59; Mismatches 119; Indels 88; Gaps 18;

QY      18  RRVLLSSRLLOQDRVPTTCHSTSEPRCFDPDGSGSP-ATWDFNGIWNRIDEPIL 76
Db      26  RRRPRFQTVMHEDWEK--NCKRSQKEALATRY----SSIPRSSREDFS--DQNYD---- 72
QY      77  LPSIKYGRPIKISLENVGCSAQIGKKEKNE-----RFPQAULTDEVLYFA 124
Db      73  -----VSPRYGVSVCGRRMEDAVAIHPSFSSPKNSFFPQ-----HYFG 114
QY      125  VYDGHGGPAAADFCHTHWEKICMDLLPK-----EKNLETLLTAFLEIDK-----AFS 172
Db      115  VYDGHGCSHVAARCRERHLKQVEELSDMEDEESWKTMTERSFTFRMDKEVYVSWGDSVVT 174
QY      173  SHARLSADATLITS-GTTATVALLRDGIELVVASVGDSSRAILCRKGKPMKLTIDHTPERK 231
Db      175  ANCKDLQTFACDSVGSTAVSVITPD-KIVVANGDGRAVLCRNGKPVLTSTDKHPDRP 233
QY      232  DEKERIKKGGG-FVAVNSLGFPHVNGRLANTRSIGDLDLKTSVGTAEPE---TKRIKLHH 287
Db      234  DELDRIEGAGGRVIYWDG--FRLVGLVLAWSAIGDNLKPY-VSCSEPVTTIDR----- 284
QY      288  ADSDFVLVTTDGINFMVNSQETCDFVQC-----HDP-----NEAAHAVTSEA 330
Db      285  RDDDCILASGLDWDVYVNSKACSVARMCRLGGRGRQDNEPAISDKTACTEASVLLTKLA 344

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QY 331 IQYGTEDNSTAVV 344
 Db 345 LARSSDNVSVVVI 358
 RESULT 8
 H96700
 protein F12A21.5 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H96700
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 anser, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H96700
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-464 <STO>
 A:Cross-references: GB:AF005173; NID:g11072032; PIDN:AAG28911.1; GSPDB:GNO0141
 C:Genetics:
 A:Gene: F12A21.5
 A:Map position: 1
 Query Match 16.7%; Score 326; DB 2; Length 464;
 Best Local Similarity 31.2%; Pred. No. 1.2e-19;
 Matches 99; Conservative 47; Mismatches 107; Indels 64; Gaps 11;
 QY 96 GCASQIGCKRKNEDRFDAQL---TDRVLVAVYDGHGGPAAADFCHTHMEKICIMDLLP- 151
 Db 122 GVSNRGKKGMETHTRIVCLVGNSSKSFVTDHGGKAAEFVAENLHKYVEMMEN 181
 QY 152 ---KEKNLETLTLAFLEIDKAFSSHARLSADATLTSGTTATVALLRDIQLVAVSGD 208
 Db 182 CKGKEEKVEA-FKAAFLRTDRDLEKVKQSLKGVVSGACCVTAIVDQ-EMIVSNLGD 239
 QY 209 SRALCRKPKMKLTIDHTPERDEKERIKK-----CGGFVAVNSLQCPHNGR 257
 Db 240 CRAVLCRAGVAEALTDHKKPRDDEKERIESQLIPMTFGLQGGYVD-NHOGAWRVQGI 298
 QY 258 LAMTRSIGDLDLKTSIGVIABPEYKRIKLHADDSDFLVLTDDGINFMVNSQE----- 308
 Db 299 LAVRSIGDAHLK-KWVVASPEYTRVLELEQ-DMEFLVSLASDGLWDVVSNOEAVYTVLHVL 356
 QY 309 -----ICDFVNOCHDPN-----EAAHVAITEQAIQYGTEDNSTAVVPG 347
 Db 357 AQRKTPKSEENLVQGFVAVNSPSSKLRASLVKSPRCAKSSQSYNNSESPSL----- 411
 QY 348 AWGKYKNSEINFSPRS 364
 Db 412 -----NREIGSSPSKS 422
 RESULT 9
 S41854
 phosphoprotein phosphatase (EC 3.1.3.16) PTC1 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein D2925; protein serine/threonine phosphatase; protein YD8119.0
 C:Species: Saccharomyces cerevisiae
 C:Date: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 21-Jul-2000
 C:Accession: S41854; S52513; S50976; S67538
 R:Maeda, T.; Tsai, A.Y.M.; Saito, H.
 Mol. Cell. Biol. 13, 5408-5417, 1993
 A:Title: Mutations in a protein tyrosine phosphatase gene (PTP2) and a protein serine/thr
 A:Reference number: S41854; MUID:93360976; PMID:8395005
 A:Accession: S41854
 A:Molecule type: DNA
 A:Residues: 1-281 <MAE>
 A:Cross-references: EMBL:L14593; NID:g402502; PIDN:AAA34920.1; PID:g402503
 R:Andre, B.; Vissers, S.; Urrestarazu, L.
 submitted to the EMBL Data Library, February 1995
 A:Description: The sequence of a 42 kb segment located on the left arm of chromosome IV i
 A:Reference number: S52492
 A:Accession: S52513
 A:Molecule type: DNA
 A:Residues: 1-281 <AND>
 A:Cross-references: EMBL:Z49432; NID:g683669; PID:g683691
 R:Murphy, L.; Richards, C.; Gentles, S.; Harris, D.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: S50976
 A:Accession: S50976
 A:Molecule type: DNA
 A:Residues: 167-281 <MUR>
 A:Cross-references: EMBL:Z49008; NID:g642799; PID:g642800
 R:Urrestarazu, L.A.; Andre, B.; Vissers, S.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67535
 A:Accession: S67538
 A:Molecule type: DNA
 A:Residues: 1-281 <URP>
 A:Cross-references: EMBL:Z74054; NID:g1430964; PID:e253189; PID:g1430965; MIPS:YDL006W
 C:Genetics:
 A:Gene: SGD:PTC1
 A:Cross-references: SGD:S0002164; MIPS:YDL006W
 A:Map position: 4L
 C:Keywords: phosphoric monoester hydrolase
 Query Match 16.7%; Score 325; DB 2; Length 281;
 Best Local Similarity 32.8%; Pred. No. 7.3e-20;
 Matches 79; Conservative 48; Mismatches 82; Indels 32; Gaps 7;
 QY 122 YFAYVDHGGPAAADFCHTHMEKICIMD--LLPKKNLETLTLAFLEIDKAFSSHARLSA 179
 Db 53 YFAYVDHAGHQAQSKWCGKHHTIEQNLADETRDVRDVLNDSFLAIDEINT----- 106
 QY 180 DATLTSQTATVALLR---DGI-----ELVVASVGDSSRAILCRKPKMKLT 223
 Db 107 -KLGVNSGCTAAVCVLRWELPDSVSDSDMDLAQHQKLYTANVGDSTRIVLFRNGNSIRLT 165
 QY 224 IDHTPERKDEKERIKKCGGFVAVNSLQCPHNGSLAMTRSIGDLDLKTSIGVIAPEPKRI 283
 Db 166 YDHKASDTLEQVRVEQAGGLIM----KSRVNGMLAVTRSLGD-KFFDSLVVSGSPFTTSV 219
 QY 284 KLHADDSDFLVLTDDGINFMVNSQEICDFVNOCHDPNEAAHVAITEQAIQYGTEDNSTAVV 343
 Db 220 EI-TSEDKFLILACDGLWDVDDQDACELIKIDTEPNEAAKVLVRYALENGTTDNTVWV 278
 QY 344 V 344
 Db 279 V 279
 RESULT 10
 T01361
 probable protein phosphatase 2C At2g34740 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001
 C:Accession: T01361; D84760
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
 submitted to the EMBL Data Library, May 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
 A:Reference number: Z14179
 A:Accession: T01361
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-239 <ROU>
 A:Cross-references: EMBL:AC003096; NID:g3132469; PID:g3132471
 A:Experimental source: cultivar Columbia

R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, I.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; NUID:20083487; PMID:10617197
A:Accession: D84760
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-239 <STO>
A:Cross-references: GB:AE002093; NID:g3132471; PIDN:AA016260.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g34740; T29P13.5
A:Map position: 2
A:Introns: 46/3; 139/1; 190/3

Query Match 16.5%; Score 322.5; DB 2; Length 239;
Best Local Similarity 34.3%; Pred. No. 9.5e-20;
Matches 81; Conservative 48; Mismatches 80; Indels 27; Gaps 7;
QY 123 FAVYDGHGCPAARDCHTHMEKCINDLIPKKNLETLTLA-FLEIDKAFSHAELSADA 181
DB 20 YAFDGHGSDVADYLNHL-----FNLISQDPDFWNPKKAKRAYKSTDD 66
QY 182 TLLTS-----GTTATVALLRDGIELVAVSGDSRAILCRKGPMMK-LTIDHTPERKDEK 234
DB 67 YILNVGPRGSTAVTAIVDGKXIVANVGDSRAILCRSDVYKQITVDHEPDK--ER 124
QY 235 ERIKKGCGFVAVNSLQGHVNGRLAMTRSIGDLKTS-GVIAEPTKRIKLUHADDSEFL 293
DB 125 DLVKGKGFVSQKPGNVRVDQLAMTRAFSGGGLKEHISVIPNTEIAEI---HDDTKFL 181
QY 294 VLTDTGIMFVNSOELCDPVNOCHPDNEAAHAAVTEQATQYGTEDNSTAVVFPFGAW 349
DB 182 ILASDGLWKMNSDEVDQIKRGNAEAAKMLIDKALARGSKDDISCVVVSFLQW 237

RESULT 11
T48123
Hypothetical protein F16M2.190 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48123
R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, M.
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24459
A:Accession: T48123
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-816 <RIE>
A:Cross-references: EMBL:AL139648
A:Experimental source: cultivar Columbia; BAC clone F16M2
C:Genetics:
A:Map position: 3
A:Introns: 4/1; 74/1; 162/2; 197/3; 245/1; 332/2; 454/1; 480/3; 526/1; 578/2; 639/3; 772
A:Note: F16M2.190

Query Match 16.5%; Score 322.5; DB 2; Length 816;
Best Local Similarity 27.5%; Pred. No. 5.1e-19;
Matches 112; Conservative 47; Mismatches 100; Indels 149; Gaps 14;
QY 79 PSIKYKPIPKISLENVG-----CASQIGKREKED-----REFDQALT-- 117
DB 19 PAVFQSPKCFRWLQNWGSPTHSGAGRCHTAATQGRNRYQEDRLCALDLRPPFGKGT 78
QY 118 -DEVL--YFVAVDGHGCPAAADFC-----DILLPKKNLETLTLAFLFIDKAPSS 138
DB 79 PKDLVGLIAAVFDGHGABASDMASKLLDYFALHINFLDLATFSAMTRKLGIFRPTKGD 138
QY 139 -----HTHMEKCM-----DILLPKKNLETLTLAFLFIDKAPSS 173
DB 139 HSVILHGVRDEIMHLYNLDQFQPRDSPLPHFDPSLPLDIMKALLR-AIHDDIVTFTK 197

QY 174 HAELSADATLTSCTTATVALLRDGIELVAVSGDSRAILC----- 214
DB 198 -----EASNRKLSGSTATIALIADG-OLMVASIGDSKALLCSKFTLEBEARATLVKLYR 252
QY 215 -----RKGKPMK-----LTIDHTPERKDEKRIKKGCGFVA-WNSL 249
DB 253 ERRNRGSSPSRSDFKLEHGNGLLRFIAKELTKDHPNREDEKIRVEAAGGVVTEM--A 310
QY 250 GQPHVNGRLAMTRSIGDLKTS-GVIAEPTKRIKLUHADDSEFLVLTDTGIMFVNSOEL 309
DB 311 GVPVNGQLTVSAIGDLTVRSYGVISAPEVMDWQPLVANDSLFVSSDGFLEKLEQVEV 370
QY 310 CDFVNOCHDNEA-----AAHAAVTEQATQYGTEDNSTAVVVP 345
DB 371 CDLLMEVNNQTSAGAGVPSYCSISLADCLVNTAFKSGMDNMAVVVP 418
RESULT 12
P96752
Protein phosphatase 2C (At2P2C-HA), 19519-17666 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: P96752
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; NUID:21016719; PMID:11130712
A:Accession: P96752
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-511 <STO>
A:Cross-references: GB:AE005173; NID:g6648151; PIDN:AAF21151.1; GSPDB:GN00141
C:Genetics:
A:Gene: F28P22.4
A:Map position: 1

Query Match 16.5%; Score 322; DB 2; Length 511;
Best Local Similarity 30.8%; Pred. No. 2.9e-19;
Matches 100; Conservative 49; Mismatches 102; Indels 74; Gaps 12;
QY 96 GCASQIGKREKEDRF---DEAQLTDEVL-----YFVAVDGHGCPAA 134
DB 191 GTVSIQGNRSEMEDAFVSPHFLKLPKMLMGHMGSPSLHTLTHGFFGVYDGHGKHV 250
QY 135 ADPCHTHMEKIMDLPKKN-----LETILTALFLFIDKAF----- 171
DB 251 ADYCDRLHFALEAIEIRIKDELCKRNTGEGRQVQMDKFTSCFLTVDGIEGKIGRAVV 310
QY 172 -SSHARLSADATLTSCTTATVALLRDGIELVAVSGDSRAILCRKGPMMKLTIDHTPER 230
DB 311 GSSDKVLEAVAS-ETVGSTAVVALVCS--HIVVNSCGDSRAVLFRGKAMPLSDVHDPDR 368
QY 231 KDEKERIKKCGG-FVAVNSLQGHVNGRLAMTRSIGDLKTS-GVIAEPTKRIKLUHAD 289
DB 369 EDEVARIENAGGKVIQWGG--ARVFGVLAWSRSIGDRYLKPY-VIPEVTFMP-RSRE 423
QY 290 DSFLVLTDTGIMFVNSOELCDFVQ-----CHDPN-----EAAHAAVTE 328
DB 424 DECILIASDGLWDMVNNQVECTARRRILMWHKKNAGAPPLAERKGDIDPACQAAADYLSM 483
QY 329 QAIQYGTEDNSTAVVVPFGAWKVK 353
DB 484 LALQXGSKDNISIIVIDIKAKQKFK 508

RESULT 13

A56058
phosphoprotein phosphatase (EC 3.1.3.16) 2C - fission yeast (Schizosaccharomyces pombe)
C/Species: Schizosaccharomyces pombe
C/Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 18-Feb-2000
C/Accession: A56058; T41353; T38827
R/Shiozaki, K.; Akiyama-Niaki, H.; McGowan, C.H.; Russell, P.
Mol. Cell. Biol. 14, 3742-3751, 1994
A/Title: Protein phosphatase 2C, encoded by ptc1(+), is important in the heat shock resp
A/Reference number: A56058; MUID:94254832; PMID:8196617
A/Accession: A56058
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-347 <SH>
A/Cross-references: GB:126970; NID:9497784; PID:AAA33327.1; PID:9497785
A/Note: authors translated the codon GAT for residue 51 as Asn
A/Note: in the authors' translation residues 51-60 are shown after residue 80, and resid
R/Barrell, B.G.; Rajandream, M.A.; Quail, M.; Harris, D.; Lyne, M.
submitted to the EMBL Data Library, June 1999
A/Reference number: 221814
A/Accession: T41353
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-347 <BA2>
A/Cross-references: EMBL:AL117389; PID:CA55768.1; GSPDB:GN00068; SPDB:SPC4F11.02
A/Experimental source: strain 972h-; cosmid c4F11
C/Genetics:
A/Map position: 3
A/Keywords: magnesium; phosphoric monoester hydrolase

Query Match 16.5%; Score 321.5; DB 2; Length 347;
Best Local Similarity 28.8%; Pred. No. 1.9e-19;
Matches 98; Conservative 56; Mismatches 135; Indels 51; Gaps 11;

Qy 27 LQDDRVTPTCHSTSEPCSPDPGSGSPATWDFGNWNRIDEPILLPSIKYKRP 86
Db 11 LLEPHLKNPFSNSSTGHRKNASDHSADGE-----TRPIAIEKDSKNGT 56

Qy 87 IP-----KISLNVCSAQIGK--RKENEDR----FDPAQLTDEVLYFAVYDGGGPA 133
Db 57 VPVGNSPRSKASNLWAGLMEDKQWRWSMEDTHICLYDFGQNDG--FVAVYDGGAGTQ 115

Qy 134 AADFCHTHMEKCNMLPKPKN--LETLTLTFLAFLDK--AFSSHARLSADAFLLSGTT 189
Db 116 ASDYCKQNLKLVLEKVRNPDRLVTLMDLTFVFNKIAKATHNDI-----CGCT 167

Qy 190 ATVALL-----RGIELAVASGDSRAILCRKCKPKLTIDHTPERKDKERIKKCGGFV 244
Db 168 AAVAFRYEKNRTRRVLYTANAGARIVLCRDGRALRLSYDHKGSANRRVQTQGLM 227

Qy 245 AMNSLGOPHYNGRLAMTRISGDLTKTSGLVIATPETHKRLKHADDSFLVLTDDGNFMV 304
Db 228 VQN-----RINGVLAVTRALGDTYKEL--VSAHPFTTETRIWNGHDEFFRIACDGLWDVV 281

Qy 305 NSQICDFVQCHDPNPAHAHVTEQALQYGTEDNSTAVVV 344
Db 282 SDQEAVDVFRNFSPREAAVRLVEFALKRLSTDNITCIIV 321

RESULT 14
H84543
Probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C/Accession: H84543
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eissen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A/Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: H84543
A/Status: preliminary

A/Molecule type: DNA
A/Residues: 1-355 <STO>
A/Cross-references: GB:A5002093; NID:54559345; PIDN:AAD23006.1; GSPDB:GN00139
C/Genetics:
A/Gene: At2g25070
A/Map position: 2
C/Superfamily: human phosphoprotein phosphatase 1A

Query Match 16.4%; Score 320; DB 2; Length 355;
Best Local Similarity 30.8%; Pred. No. 2.7e-19;
Matches 96; Conservative 44; Mismatches 104; Indels 68; Gaps 9;

Qy 96 GCASQIGKRNED--RDFPAQLTDEVLYFAVYDGGGPAADFCHTHMEKCNMLLPKE 153
Db 25 GLSSMQGWRATMEHAAILDLDDKTSTFFGYDGGKVAKFCAYLHQOVSNEAYKT 84

Qy 154 KNLETLTLTFLAFLDK--AFSSHARLSADAFLLSGTT-----GTTATVALLRDGLVV 203
Db 85 GDVETSLRRAFRVDDNMQGGWRGLAVLGDKNKFTSGMIEGFIWSPRSGDTNNQPDW 144

Qy 179 -----ADATLLTSGTTATVALLRDGLIELVAVSGDSRAILCRKCKPKLTIDHTPERK 231
Db 145 FLEDGPHSDFTGPTSGCTACVALIKDK--KLFVANAGDSRCVISRKSQAYNLKDKHDPLE 203

Qy 232 DEKERIKKCGGFVAVNSLQGPVHNGRLAMTRISGDLTKTSG-----VIABPETKRI 283
Db 204 VEKERILKAGGFI-----HAGRINGSNLNTRAGDMFEFKQKFLPSEKQWVADPDINTI 258

Qy 284 KLHADDSFLVLTDDGNFMVNSQEI CDVFNQCHDPNPAHAHVTEQALQYGT----- 336
Db 259 DLCD--DDDFLVVACDGIWDCMSQELVDFIHEQLKSETKLSTVCEKVVDRCLAPDTATGE 317

Qy 337 --DNSTAVVVPF 346
Db 318 GCDNMTIILVQF 329

RESULT 15
T05095
Hypothetical protein F28M20.60 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C/Accession: T05095
R/Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes, F.
submitted to the Protein Sequence Database, November 1998
A/Reference number: 215398
A/Accession: T05095
A/Molecule type: DNA
A/Residues: 1-389 <BEV>
A/Cross-references: EMBL:AL031004
A/Experimental source: cultivar Columbia; BAC clone F28M20
C/Genetics:
A/Map position: 4
A/Introns: 95/1; 128/1; 181/1; 210/1; 274/3; 318/3
A/Note: F28M20.60
C/Superfamily: human phosphoprotein phosphatase 1A

Query Match 16.4%; Score 319.5; DB 2; Length 389;
Best Local Similarity 30.8%; Pred. No. 3.3e-19;
Matches 97; Conservative 45; Mismatches 92; Indels 81; Gaps 11;

Qy 96 GCASQIGKRNED--RDFPAQLTDEVLYFAVYDGGGPAADFCHTHMEKCNMLLP 151
Db 60 GYASPGKRSMEFYETRIDGVE--GEIVGLFGVDFGGRGARAAYVKQNL---FSLIR 115

Qy 152 KEKLETLTLTFLAFLDKAFSSHARLSADAFLLSGTT-----GTTATVALLRDGLVV 203
Db 116 HPK-----FISDTTAAIADAYNTDSEFLKSENSQNRDAGSTASTAIL--VGDELLV 165

Qy 204 ASVGDSRAILCRKCKPKLTIDHTPERKDKERIKKCGGFVAVNSLQGPVHNGRLAMTRIS 263
Db 166 ANVGDSRAVICRGNAIVASRDHKPDQSDERQRIEDAGGFVW--AGTWVGVGLAVSRA 223

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QY 264 IGDLDLKTSGVIAEPE-----TKRIKLH----- 287
Db 224 FGRLLK-QYVADPEIQVLTFCQNLLEYKNATLLLTIEHNLHWISVYINGTLQNFL 282
QY 288 -----ADDS--FLVLTDDGINFVNSQEICDFVNOCHDPNEAAHAYTEQAI 331
Db 283 RSLISINGKFBEEKVDSSLEFLILASDGLWDVVSNEEAVGMIKATEDPEGAKRLMMEAY 342
QY 332 QYGTEDNSTAVVVPF 346
Db 343 QRSADNITCVVVR 357
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Search completed: October 12, 2004, 05:58:49
Job time : 39 secs

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